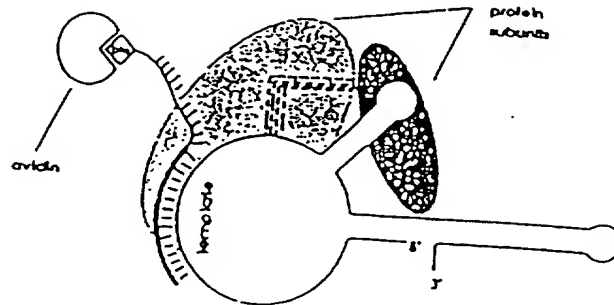


PANEL A



PANEL B

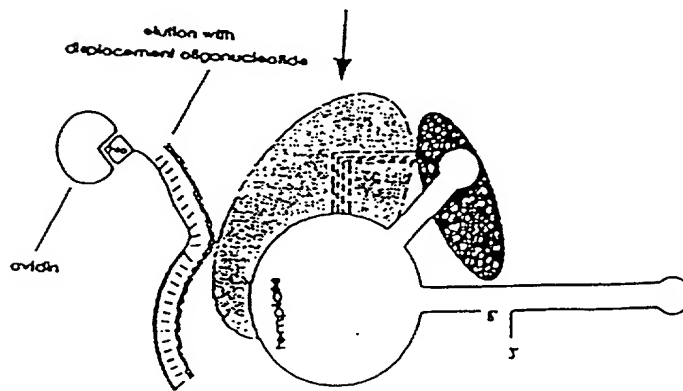


FIGURE 2

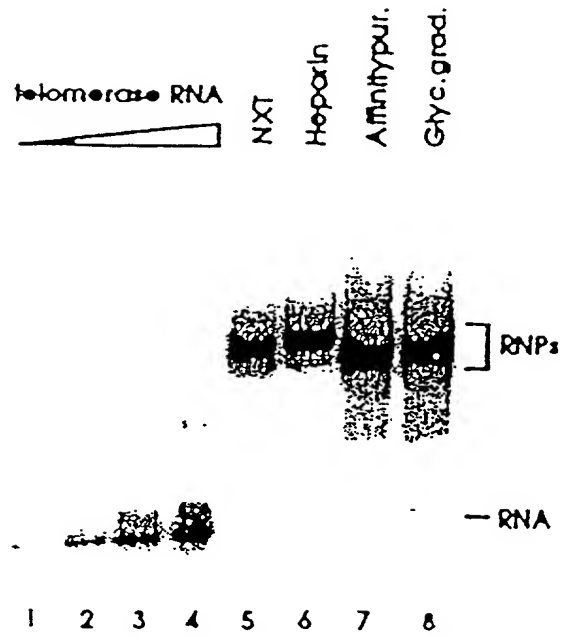


FIGURE 3

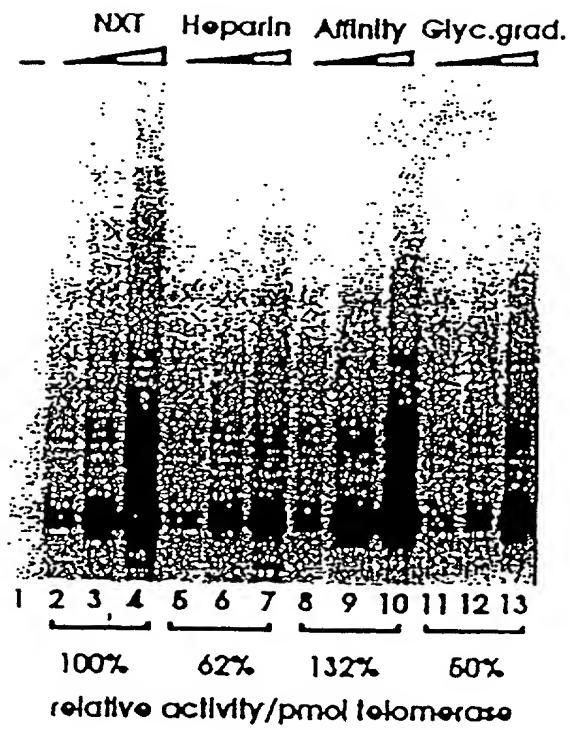


FIGURE 4

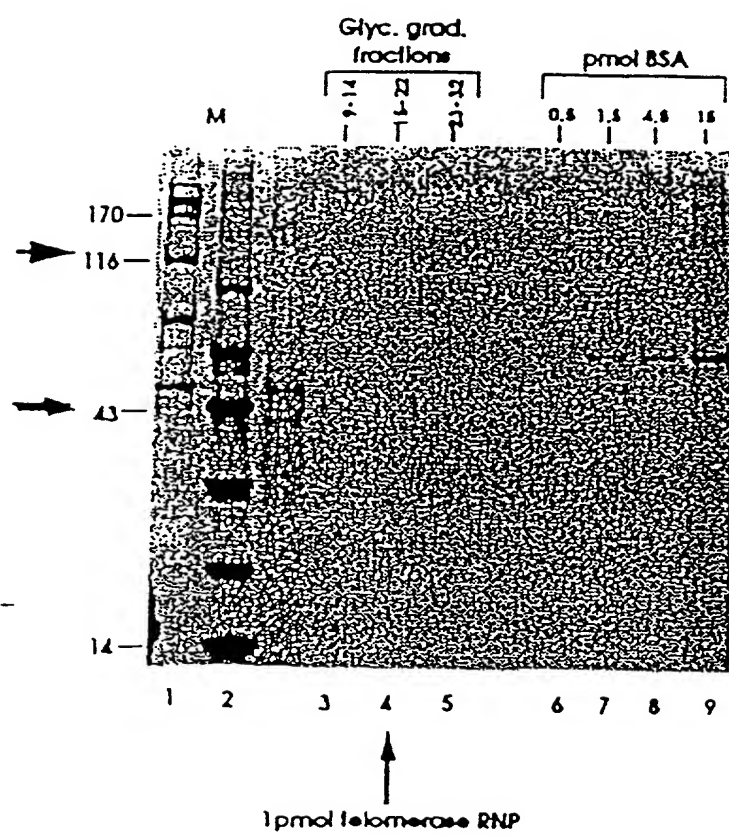


FIGURE 5

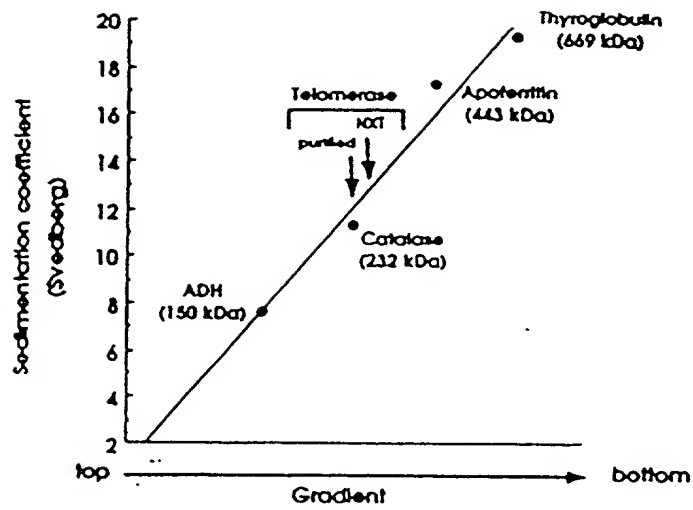


FIGURE 6

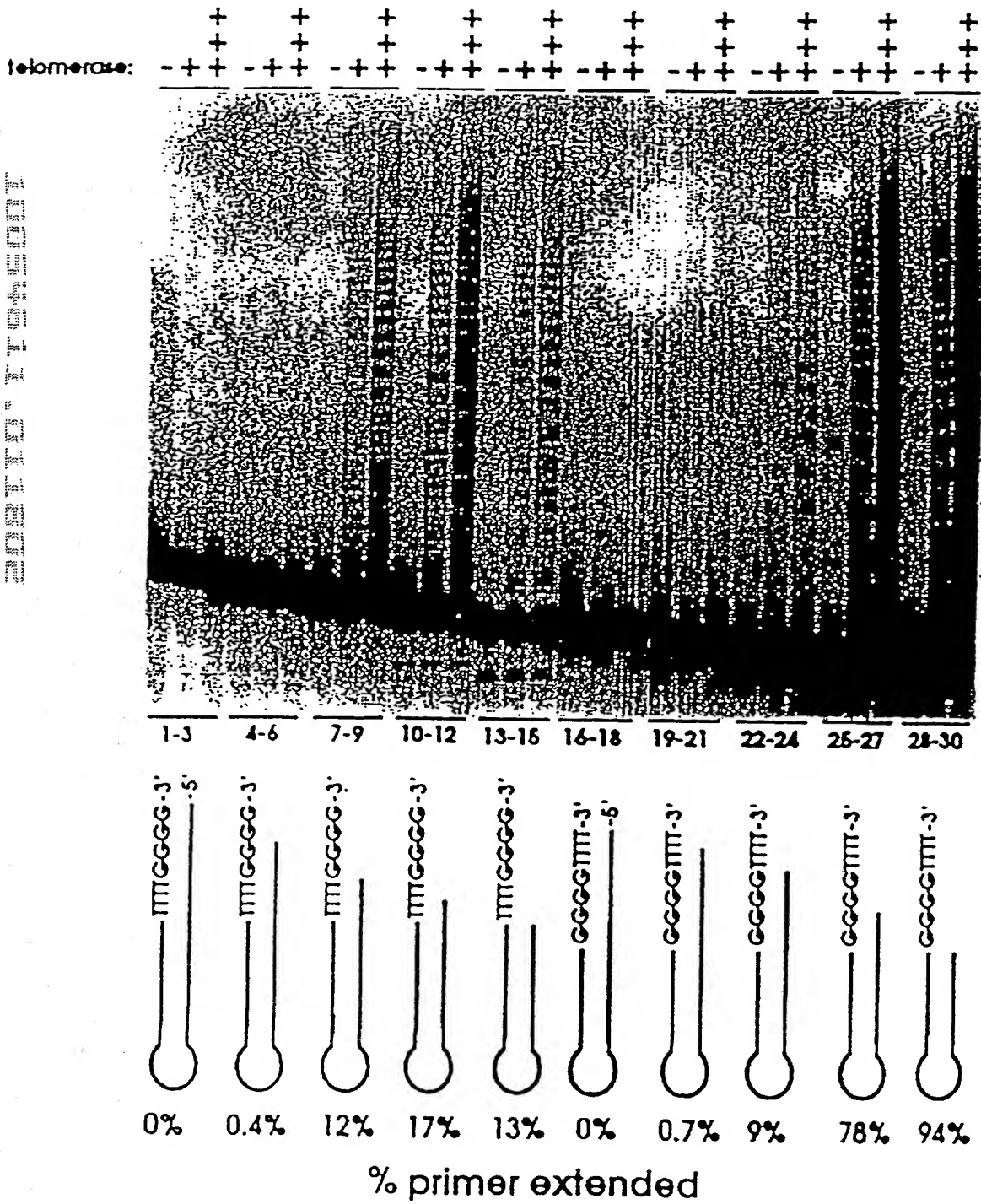


FIGURE 7

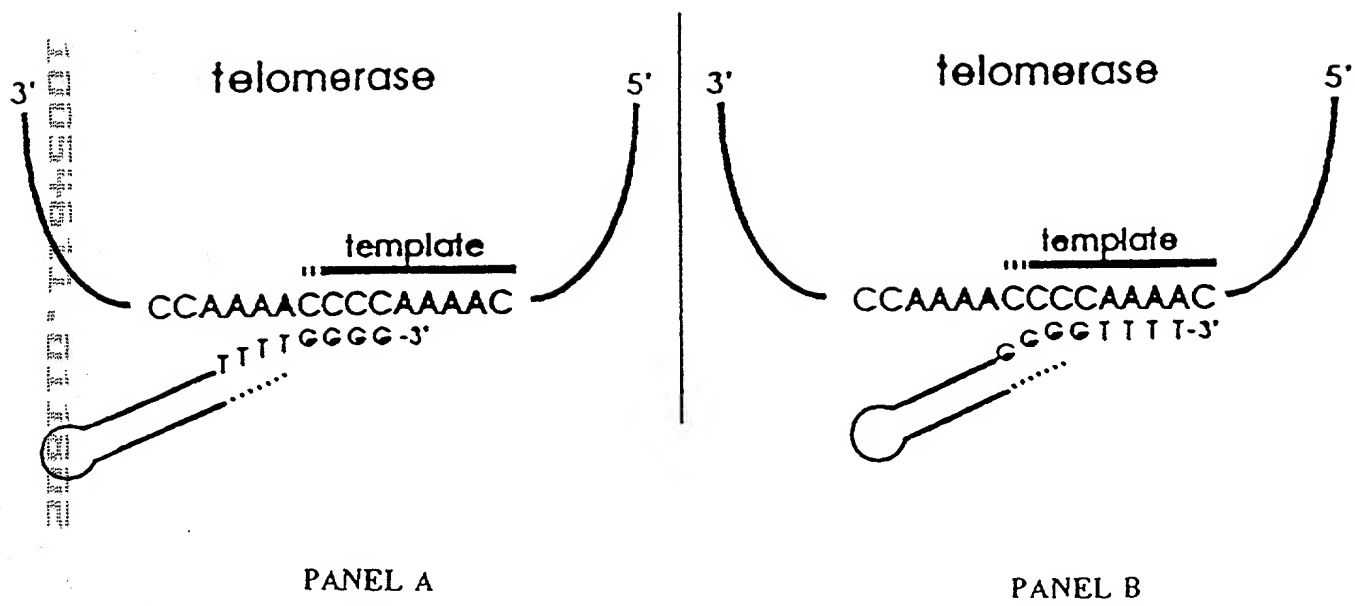


FIGURE 8

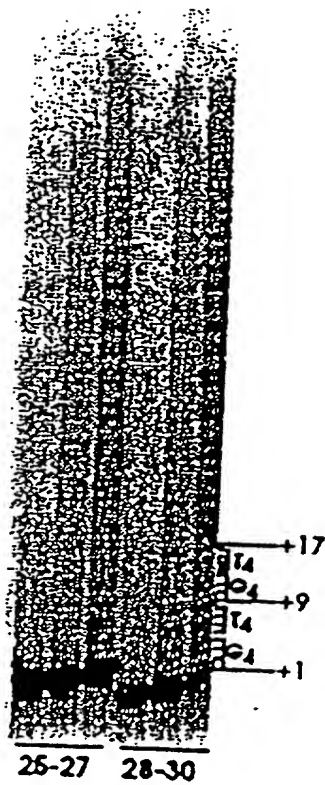


FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TAAAAATATT TGCGCAGACA AATATTGTTG CTA CTCTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGA ACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTC
 501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCTCTTCCA GAAAATTGGC GGAACGGAA ACAAAAAATC GAAA ACTTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
 1151 TACACA ACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAGT TAAGAAATAT GTGGA ACTAA ACAAGCATGA ACTCATTCAC
 1301 AAAA ACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGTTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
 1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTCAGA CCGGAAGACT ACAA AATTAA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
 1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
 1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAA ACTATC
 1951 AACATTCTTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
 2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
 2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
 2251 CCAATATAAT TACATTA ACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACCTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTA AAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA
 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAM
 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHელი
 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501 EEWKKS LGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVDSKN
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ
 701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
 1001 KYIFNRVCM LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCCAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
 51 GTAGTTTGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTAA
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TACTATTTCG
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651 TTGAGACAAT TGAAAAAGCT GTTTACAACCT GAAGGAATCG CAGTTCTGAA
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
 1001 TTGTTGATTG TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTG TTAAGATTG CAAAAATTCC
 1101 AGGTAAGAGA GATACATTCA TTAAGATTG TATATTATAG TTTTTCATT
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA
 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
 1751 GGGGTTTTGG GG

FIGURE 12

CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAATTGAGGTAGTTTAGA
 1 ----- 60
 GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTCTTTTTTAACTCCATCAAATCT

a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -

AATAAAATATTATTCCTGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
 61 ----- 120
 TTATTTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y C F G C Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -

TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 ----- 180
 ATGAAGGATTATGTAAGTTGTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * * Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -

CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 ----- 240
 GTAACCTTAGACCGAGCTTTAGCGGAAGTAAGTATAAGGTTTCAACGTTTTTGTAAATC

a H C N L A R N R L H C L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -

AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 ----- 300
 TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a S S T S R M Q I F I T I L S C E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

AAAGCGGAGAGCAAGAGTAAATTTGAAACATTACTAATGTTTAAATAAATCAGGTAA
 301 ----- 360
 TTTCCGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N C N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -

TGAGGATTATCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 ----- 420
 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a C G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

TACTAAAGGTAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
 421 ----- 480
 ATGATTTTCCATTGTCAAACTAATAAAGGATCGGTTGTTACTACTCATATAATTAA

a Y * K V N S L D Y F P S Q Q C C V Y * I -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T M M S I L N S -

FIGURE 12 (cont.)

481 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAACTCGCTAT 540
GTATACTCTTACTCAGTTTCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H M R M S Q R I S I H Q T Y Q R Q T R Y -
b I C E C V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L -

541 AAAACGCCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTTCG 600
TTTTCGCTTCTTTTCAAACATTAGCTTGTCTCTTCTGAATAACGTAAATGATAAGC

a K T Q E K V C * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -

601 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAAGCTCTGTTA

a Y G F Y Y N C F R Y R R C T P E S C D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -

661 TGAAAAAGCTGTTTACAACGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT 720
ACTTTTTTCGACAAATGTTGACTTCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a C K S C L Q L K E S Q F C K F * C V C H -
b E K A V Y N C R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -

721 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L C I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -

781 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T Y Q V * W N I R * I L W D K C T L -

841 TGAATTTATATTCGATTCTTAAAGCATAGATACAGAAATGCTTTAGAGACTGATTTAGC 900
ACTTAAATATACCTAAGATTTCGTATCTATGTCTTACGAAATCTCTGACTAAATCG

a C I Y I G F L K H R Y T E C F R D C F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y * I L K A * I H R M L * R L I * L -

901 TTACAACAGATTACCTGTTTTCGATTACTCTTGCTCATCTCTTATATCTTTAAAGAAGCA 960
AATGTTGCTTAATGGACAAAACATAAGAGACGAGTAGAGAATATAGAAATTTCTTCTGT

a L Q Q I T C F D Y S C S S L I S L K E A -
b Y N R L P V L I T L A H L L Y L * K K Q -
c T T D Y L F C L L L I S Y I F K R S R -

961 GGCGAAATGAAAGAAGACTAAAGAAAGAGATTTCAAATTTGTTGATTCTTCTGTAACC 1020
CCGCTTTACTTTTCTCTGATTCTTTCTCTAAAGTTTAAACAACATAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -
b A K C K E D * R K R F Q N L L I L L * P -
c R N E K K T K E R D F K I C C F F C N R -

1021 GGAATTAACAACAAGATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC 1080
CCTTAATTGTTGTTCTTAATCGTTGCTTTTCTTCTCTCGATAGTGTAGGACTAAG

a C I N H K N : S N E K E E E L S Q S C F -
b E L T T R I L A T K K K K S Y H N P D S -
c N * Q Q E Y * Q * K R R R A I T I L I L -

FIGURE 12 (cont.)

1081 TTAAGAGTTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAAATTCATATATTATAG 1140
AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L -
b R F Q K F Q V R E I H S L K F I Y Y S -
c K D F K N S R E R Y I H N S Y I I V -

1141 TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA 1200
AAAAAGTAAAGTTCGACAATAAAAGAAAAATAGAATTGTTATAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D L E -
b F S F H S C Y F L L S Q Y F L I S W K -
c F H F T A V I F F Y L N N I F C L A G S -

1201 GTAAAAAGTATCAATAAGAGAAGCGCTAGACTGAGGTAACCTTAGCTTATTCACATTCAT 1260
CATTTTTCATAGTTTATTCTCTTCGGCATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a V K S I K E K R T E V T L I H I H -
b K V S N K R S A R L R L S L F T F I -
c K K Y Q I R E A L D C G N L A Y S H S -

1261 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA 1320
TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTT

a R S T F I Y P I R C G N S S H P F K -
b D R P S Y I Q Y D D K E T A V I R F K N -
c I D L H I S N T M I R K Q Q S S V L K I -

1321 TAGTGCTATGAGGACTAAATTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA 1380
ATCAGGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAAATAGTTTTT

a C Y E D I F R V K K W S R N L N Q K -
b S A H R T K F L E S R N G A E I L I K K -
c V L C G L N F S Q E H E P K S S K R -

1381 GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTGTTAATAAGTATTACCA 1440
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L I F R V L P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S I L Q K N R T L N L S L I S I T N -

1441 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA 1500
TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTCTTCTAGTAATTTCTTTATTT

a I L I D C R D R G N C T E D H R N K -
b S C L I E E I D E A T A Q K I I K E I K -
c L D C L K R L T R Q L H R R S L K K S -

1501 GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA 1560
CATTGAAATTAATTAATCTCTTATTGATTAAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N R I N I T N I E I S D L Q -
b L L L I R E T K L L I R S A I F N -
c N F Y L E N K L N Y Y R D Q R S S I -

1561 TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT 1620
AACTGCTTTATTTTCGACTTGATTCAATCTGTTATTTTTTATGTTTGAACCAAGTTTA

a L T K K L N S T I K N T N L G Q N -
b C R N K S C T K V R Q K I Q T L V K I -
c D E I K A E L K L D N K K Y K P W S K Y -

1621 ATTGAGGAAGCAAAAGAAGACCACTTAGCAAAAAGAAAAATAAGCGCAATAAATAAAATGA 1680
TAACTCCTTCCTTTCTTCTGCTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R O I K C -
b L R K E K K T S Q K K K G N K N E -
c C G R K R R P V S K R K N X A I N K H S -

FIGURE 12 (cont.)

1681 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTCATAATTTATTGAAAAGAGGGGTT 1740

CATGCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAATAACTTTTCTCCCAA

a V Q K C R N K R F I F F N N L L K R G V -
b Y R S E E I K D L F F S I I Y C K E G F -
c T E V K K * K I Y F F Q * F I E K R G F -

1741 TTGGGGTTTTGGGGTTTTGGGG 1762

AACCCCAAAACCCCAAAACCCC

a L G F W G F G -
b W G F G V L G -
c G V L G F W -

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FIGURE 13

2 EVDVONQADNHGHSALKTCCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL 51
 19 ELELEMEQENQNDIQVRVK...IDDPKQY...LVNVTAACLLQEGSYQDK 62
 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF...STGLMIELIDKCLVELL 100
 63 DERRVITKALL...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF... 107
 101 SSSDSVDRQKLQCFGFQKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
 108 CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144
 151 IGNEFRHLYTKYLIFORTSEGTLVQFCGMNVFDHLKVNDKFDKKQKGA 200
 145 FDATEFNKLY...LDRILSQDIRKELTFRKCLQRCVRSKF 181
 201 ADMNE PRCCSTCKYNVKNKDHFLNNINVPNNNMKSRTTRIFYCTHF 247
 182 SEFNEYQLGKYCTES...QRKKTMPRYLSVTNKQKWDQTKK... 220
 248 NRMNQFFKKHEFVSNKNNISAMDRAQITFTNIFRNRIRKKLKDVKIEKI 297
 221 RKENLLTKLOAIKESDKSKRETG...DIMNVEDAIALKPAVMKKI 264
 298 AYMLEKVKDFNFNYLTKSCPLPENWRERKQKIENLINKTREETSKYYEE 347
 265 AKRQAMK...KHMKAPKIPNSTLESKYLTTFKD 294
 348 LFSYTTDNKCVTQFINEFFYNILPKDFTGRNRKNFQKKVKKYVELNKHE 397
 295 LIKFCHISEP...KERVYKILGKKYPKTEEEYKAAFQDSASAPFN...PE 338
 398 LIHKNLLEKINTREISWMOVETSAKHFFYFDHENIYVLWKLRLWIFEDL 447
 339 LAGKRMKIEISKWENELSAKNTAEVWONLISSNQLPYMAMLRNLSN... 386
 448 VVSLRCFFVYTEQKQSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
 387 ILKAGVSD... 394
 498 KEVEEWKKSGLGFAPGKRLRIPKKTFRPIMTFNKKIVNSDRKTKLTNT 547
 395 TTHS 398
 548 KLLNSHMLKLTKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGPKL 597
 399 IVINK...ICEPKAVENSKM 415
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNIVID 647
 416 F...PLOFFSAIEAVN...EAVTKGFKAKK...RENMNKQIEAVKE...VVE 457
 648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKT LIVE 697
 458 KTDEEKDQM...ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496
 698 AKQRYNFKKDNLLQPVINICQYNYINFNGKFKYQTKGIPQGLCVSSILSS 747
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLECALVLGL 546
 748 FYYATLEESSLGLFRDESMNPENPNVNLMLRLTDDYLLITTQENNAVLFI 797
 547 MVKQRCCKSSFYIFSSPSSQCNKCYLEVDL... 576
 798 EKLINVSRENGFKFNMKK...LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
 577 PGDEL RPSMQKLLQEKGLGGG...TDFPYECIDEWTKNKT HVD 617
 847 WIGISIDMKTLALMPNINLRIEGILCTLNLMQTKKASMWLKKKLSFLM 896
 618 NIVILSDMMIAEGYS DINVRGSSIVNSI...KKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGGYKYMOCAYEKD...HFKNLAM 945
 654 PNKIF...AVDLEGY...KCLNLGDEFNENNYIKIFGM 687
 946 SSHIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFI 995
 688 SDSI...LKFISAKQGA...NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI...KNFALQKIG 717

[illegible]

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1  MEMDIDLDDIENL . . . LPNTFNKYSSSCSKDKGCKTLKSGSKSPS . . . 42
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491 IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSHSGGAKKYGSVRTCLEC 540
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43  LTIPKLOKO . . . LEFFYSDANLYNDSFLRKLVLKSGEORVEIETLL 85
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541 ALVLGLMHVKQRCEKSSFYIFSSPSSQCNCYL . EVDLPGEDELPSMQKLL 589
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	Motif A	Motif B
Consensus	h--h <h>h</h> h--h--h	h---+ <h>h</h> h---Sp
telomerase p123	Q Q KLFFATMDIEKCYDSVNREKLSTFLKTKLL-100-KFYKQTKGIF h CLCVSSILSSFFYATLEESSLGFL	
Dong (LINE)	KNRNLHCTYIDYKKA ¹ FD ² SI ³ PHS ⁴ VLIOVLEIYKIN-28-RQIAIKKGIY h CDLS h PFJWFCLALNPLSHQLHNDR	
al S.c. (group II)	FGGSNWFFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGP ¹ RVCV h CA h PTSPALCNAVLRLRRLRRLAGLA	
HIV-RT	LKKKRSVTVL h VGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLF h CKWKG h SPAI h FQSSMTKIL h EPFRKQN	
L8543.12	VLPELYFMK h FLVKSCYDSIPRMECMRILKDALKN-68-KCYIREDEGLF h CESS h LSA h PIVDLVYDDLL h EFYSEPK	

	Motif D	Motif E
Consensus	h h--h--h	h-h h h--h
telomerase p123	-14-LMRLTDDYLLITQENN-0-AVLFI h EKLINVSREN h CFK h FN h TK h LQT-23-QDYCDW h IG h ISI	
Dong (LINE)	-16-HLIYMDI h IKLYAKNDKE-0-MKLLIDTTTIFSN h DISMQ h FL h CKT-25-KC h YKYL h GFQQ	
al S.c. (group II)	-55-YVRYAD h ILIGVLGSKN-2-KI h KADLN h FLNS h IGLTINE h ERTLI-4-ET h ARFI h GYNI	
HIV-RT	-4-IYQYMD h LYVGS h HL h EIG-1-HRT h K h DEELRQ h HL h RL h WGLTTPDR h K h HQK-0-EP h FLW h MG h YEL	
L8543.12	-8-ILKLAD h FLIISTDQQQ.....VINIKKLAM h CFQKYN h AK h ANR-41-IRSKSSK h GIFR	

FIGURE 18

telomerase p43	LQKQIEFYSDANLYNDSEERKLVLKSGEQRVEIETLLM
human La	ICHQIEYVFGDENLPRDKELKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQIEYVFGDENLPRDKELKQOI.LLDDGWVPLETMIK
Drosophila La	ILRQVEYVFGDANLNPRDKELREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKQVEFYSEFNFPYDRERRTTAEK.NDGWVPISTIAT

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FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaatt itagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt aggggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt ctgaggtgg ctgagctga tctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtttgt
 421 ccacaagaat actcaacat tcatcgaaaa gtacttcaac aaagcagtac tttgcctaa
 481 tgacttactg gaagtctgtg aattgcata ggttctctat attttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatacttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgag tcagaagcaa gttttctgaa ttcaacgaat actaactggg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttacca
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaactctgag ataagtcctaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggat caaagtactt
 961 gacctcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatccttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
 1081 tgcatctgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataattta
 1201 ttcaagcaat taactccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
 1261 cgggttttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
 1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
 1381 agttactaag ggattcaagg ccaagaagag agaaaatag aatcttaaag gtcaaatcga
 1441 agcagtaaaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
 1501 aaccgaagaa ggagaatttg ttaagtcaa cgaagggaatt ggcaagcaat acattaactc
 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca-aaggacacac
 1621 tgcaatcttc tctgatgttt ctggttctat gactaccca atgtcaggtg gagccaagaa
 1681 gtatggttcc gttctactt gtctcgagtg tgcattagtc ctgtgttga tggtaaaata
 1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
 1801 ttacttaagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aactttgca
 1861 agagaaagga aaacttggtg gtggtactga tttccctat gattgcattg atgaatggac
 1921 aaagaataaa actcacgtag acaatacgt tattttgtct gatagatga ttgcagaagg
 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
 2041 tgaagtaaat cctaactta aaactttgc agttgactta gaaggttacg gaaagtcct
 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
 2161 aatcttaaag ttacttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
 2221 ctttgccctt caaaaaatag gacaaaagtg agtttctga gattcttcta taacaaaaat
 2281 ctcacccac tttttgtt tatgtcatag ccattatgaa atttaaatia ttatctatt
 2341 atttaagta ctacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFVCVVKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFSDSASAP
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNLIKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKLGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVLDLPGDELRPSMQKLLQEKGLGGGTDFPYECIDEWTKNKTHTVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaaaactaca aagaaaatgt caaggcgtaa
 61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat ctgtatttg tattacaaaa
 121 tctagaagt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagttaat tgataaaaa agttggttct aaggtagaga aagattgaa
 361 ttgaaacgaa gatgaaaaca aaaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aatagggtta gtattaaaat ttagtatta acatggacta
 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggttgaaa tatctcatga ccaaaaaaat tatgtatcaa ttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattattt aataaaaaca attatgatca
 661 tctaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgatt
 721 ttcacaaca atcaaaacta ctaataattc ttactagact gttacatag acgttaatt
 781 tgataataat ctctgtatac tcgattgct tagatttta ttactactag aaagattcaa
 841 tattttgaat ataagattc ctatacaag aaattaatat aatttgaga aaattggtga
 901 gctactgaa actatcttcg cagttgtct ttctcatgc cactacaag gcattcatt
 961 acaagttctt tgcaagcgt tctaattt agttaactcc tcatcataa ttagcgtaa
 1021 agatagctaa ttataggat actctttctc tacagactta aaattagtg acactaaca
 1081 agtccaagat tttttaagt tctataaga attccctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtcta ctaacgctgt agagaacctc aatgtttac ttaaaaaggt
 1201 caagcatgct aatcttaatt tagttctat ccctacctaa ttcaatttg atttctact
 1261 tgttaatta taacattga aattagatt tggattagaa ccaaatatt tgacaaaaa
 1321 aaagcttgaa aatctactt tgagtataa ataatacaaa aatcttaaat ttttaagatt
 1381 aaactttac acctacgttg ctaagaac ctcagaaaa cagatattaa aacaagctac
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa cttaagatga
 1501 aactccaagc gaaagcacia gtggtatgaa atttttgat catcttctg aattaaccga
 1561 gcttgaagt ttcagcgta acttgaagc tacccaagaa attatgata gcttcacaa
 1621 actttgatt agatcaacaa atttaagaa gtcaaatta agttacaat atgaaatgga
 1681 aaagagtaaa atggatacat tcatagatct taagaattt tatgaaacct taaacaatct
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttctatg aactgacaaa
 1801 taaagattct acttttata aatttaagct gaccttaac taagaattt aacacgctaa
 1861 gtatacttt aagtagaacg aatttaatt taataacgtt aaaagtgcaa aaattgaatc
 1921 ttccāāta gaaagcttag aagatattga tagtcttgc aaatctattg ctcttgtaa
 1981 aaatttcaa aatgttaata ttatcgccag ttgctctat cccaacaata tttagaaaa
 2041 tctttcaat aagcccaatc ttctatttt caagcaattt gaataattga aaaatttga
 2101 aaatgtatc atcaactgta ttctgatca gcatatactt aattctatt cagaattct
 2161 agaaaaaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta
 2221 tcttgattat actaaattt taaaacact tcaatagta cctgaattaa attaagtta
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagtt atcaagaat catcctaac
 2401 ccttagcta atagatttg accaaaacac tgaagtgtat gacttatta aaaagatttt
 2461 agaactata tctgagtcta agtatcatca ttattgaga tgaacccta gtaacttag
 2521 cagtttaatt aaatctgaaa acgaagaat ttaagaactt ctcaagctt gcgacgaaa
 2581 aggtgttta gtaaaagcat actataaatt cctctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcagatagat ggtgattaat taaataattg tttaataaa tattaataat
 2701 tgaataattc ttgcttatt attgaataa tacataaat agtcaattt agtgtttga
 2761 atattttta gttattaat tcatatttt aagtaataa ttattttca atcattttt
 2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDVFLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHNLNVSINRLETEAE
FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLSLERFNILNIRSSYTRN
QYNFEKIGELLETFVVFVSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL
VSIPTQFNDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE
LNQVYINQQLLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD
DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP
LCLPTGTYYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR
EAIPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVDLSHLR
QSPKERVLFIIILQKLLPQEMFGSKKNKGKIIKNLNLNLLSLPLNGYLPFDSLLKKL
RLKDFRWLFISDIWFTKHNFNENLNQLAICFISWLFRLIPKIIQTFFYCTEISSTVTI
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMRJIIPKKSNNEFR
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE
FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN
TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINNVEMEIFKTALWVEDKCY
IREGDLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV
INIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF
KDLSINVTQNMQFHSFLQRIEMTVSGCPITKCDPLIEYEVRFITLNGFLESLSNTS
KFKDNIILLRKEIQHLQAYIYIYIHVN

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESLGFLRDESMNPENPNVNLLMRLT

Author	Year	Country	Sample Size	Sample Type	Study Design	Outcome Measure	Findings
Wong	1999	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2000	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2001	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2002	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2003	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2004	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2005	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2006	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2007	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2008	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2009	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2010	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2011	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2012	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2013	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2014	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2015	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2016	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2017	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2018	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2019	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%
Wong	2020	China	1000	General population	Cross-sectional	Prevalence of hypertension	10.5%

FIGURE 25

human AKFLHWLMSVYVVELLRSPFFYVTETTFQKNR
 tez1 ISEIEWLVLGKRSNAKMCLSDFEKRRQIFAEFIYWLNSFIIPILQSFFYITESSDLNR
 EST2 LKDFRWLFISD---IWFTKHNFFENLNQLAICFISWLPRLPKIIQTFFYCTEISSTVT-
 p123 TREISWMQVET-SAKHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
 . * * * *

human LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
 tez1 TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTP
 EST2 IVYFRHDTWNKLITPFIYEYFKTYLVENWVCNRNHSYTLS--NPNHSMKRIIPKKNNEF
 p123 TYYRKNIWVIMKHSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLLPKK--TTF
 . * . * . * . * . * *

human RPIVNM DYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
 tez1 RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLIN EESSGIPFKLEVYMKLLTF
 EST2 RIIAIPCRGADEEEFTIYKENHKMAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
 p123 RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGFAVFNYDDVMKKY
 * * * *

human KKDLLKHRMFOR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
 tez1 KQRLKKKFNNVLP ELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
 EST2 EBFVCKWKQVGPQLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRN
 p123 . * . * . * . * . * *

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTTGCCATTCTGCAAATGTAAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAACAATTTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCTTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCAAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAA
GGATTTTCGGTGGTTGTTCAATTTCTGATATTTGGTTTACCAAGCACAAATTTTGAAACTT
GAATCAATTGGCGATTTGTTTCATTTCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAGTAATAATGAGTTTCAAGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTATAGCGAGTTTAAAGC
CAGTCTTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCAATCAGATGATGATACGGT
TATTCATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTTCAAATCTAGTAAAGGGATATTTCAAGTTTAAAT
AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCATTGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHQREARPA LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

1054641 012302

FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAGAAGACAGGCTCTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG

10546.01332

FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLN DYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNK SARKEVSWNSISIRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LNAFQVKQLHKVIPLVSQSTVVPKRLK VYPLIEQTAKRLHRJLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKR SNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT
SMKMEAFEKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKV VQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKV GIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVD DFLFITVNKKDAKKFLNLSLRGF EKHNFTSLEKTVINFENSGIINNTFFNESKKRMPFFG
FSVNM RSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFCL
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRRJAD

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FIGURE 30

ggtaccgatttacttcttcttcataagctaattgcttctcgaacgctcctaatactctggaatattttacaagaactcaataacaataccaagtc aaattccaatatgaagg
 tgttattagtagtcgataatatttctatttaccggtcgttaccagataaggacaaaaagaacaacttcttccccctaaagacttttactttatttacttttcaaatatttctg
 ggttcgcttacttttaacggtgactgttttagctgctactcttagccaaccgctgtttctaccccgctcattggatagctcttggagtagctcacagaaatccttacaatctt
 ctgatgagactatattagattcattacagtcggtgcatacttcaacatggagccttacacttttagatgagtcacgctcgatgatggagtatttggatcatccaacggttgccttg
 aaaagggtgataattattgcaaaatcatgiccttagtggtggaatccgcgaaggtttttagcttgcacacgcttagcatgattgagatattcaaaaatttctatccactacaa
 ctctttaacgcggttttatttttctatttttctatctggttccaaatattgatcatctcgtattaggcttttttcttactcctggaatcgaccttttctactttccccctaatg
 aataatcaaatagggttcgcttataattgatagtagtagaagattgggtgattctactcgtgtaagtatttagtttaagatactttgcaaaacatttattagctatcattatataaaa
 aaaaatcctataattataaatattatcaatatttgcggtcactatttttaaaacggttatgatcagtaggacactttgcatatatatagttatgcttaattggttacttgaacttgcAT
 GACCGAACACCATAACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTAT
 CCTTAAATGATTATGTACAACTTGTGTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA
 CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTTCTTCATTTCGACTGTAGTCGGCTTCGACAGT
 AAGCCAGATGAAGGTGTTCAATTTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatatatttttggttgatttttctattc
 ggatagctaataatgggcagCTAATAGCGAATGTTGTAAAAACAGATGTTTCGATGAAAGTTTTGAGCGTCGAAGGA
 ATCTACTGATGAAAGGGTTTTCCATGgttaaggatttcaattgtgaaatatttaccgtcaattactgtttcaagagattgtatttaaccgataaagAA
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTTAATTA
 CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTAGAAATgttaataaccggttaagattgtgcgcaacttgaaca
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 CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTTAAAAATAATGTGTTTGAGGAACTGTGT
 CAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAAGAAGTTTC
 CTGGAATAGCATTTCATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAAGCAAGgt
 aactaactgtttatccttcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG
 TGGCTTCAATGGATTTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA
 AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCCTAAAGGTATACCCTTTAATTGA
 ACAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA
 CACCCACGATGATGAAAAAATCCTTAGTTATTCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC
 CATTCTTGTTGAGTGTTTCTTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTTAAAGg
 tattgtataaaatttattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC
 ATTATTTAATGAGTAACATAAAGgttaatatgccaaattttttaccattaattaacaatcagATTTTCAGAAATTGAATGGCTAGT
 CCTTGGAAGAAAGGTCAAATGCGAAAAATGTGCTTAAGTGAATTTGAGAAACGCAAGCAAATATTTGCGG
 AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC
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 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattttaatttttggatcaatgtactttacttctaacttatttag
 cagATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACCTTTACGACCTGTGGCATCGATACTG
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 TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT
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 AGCTACAAAAAATTTGTTAGTGAGGCGTTTTCTATTgttaagttatttttcttgaatttttaacaaattcttttagTTGATAT
 GGTGCTTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTTTGT
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAAAATGCTCAAGGAACATCTCTCTGGACACATTGT
 TAAGgtataaccaattgtgaattgtaataacactaatgaaactagATAGGAAATCTCAATACCTTCAAAAAGTTGGTATCCCTC
 AGGGCTCAATTCTGTCTATTTTTTGTGTCTTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT
 TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAA
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 ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC
 ATATGGGGAAATCTTTTTTTTACAAAATTTCTAAGgtataactgtgaactgaataatagctgacaataatcagATCGAGCCTTGC
 ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATATATATAG
 GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCC
 AAAGAATGTTTACAAACGGgtgagtagtatttttaactgaaaagtcattaataaccttagATCTTTTGAATGTTATTGGAAGAAAA
 ATTTGGAAGAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAA

FIGURE 30 (cont.)

ATGgtacgtgtcggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTT
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcatttcaatttattatatacatcctt
tattactgggtcttaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaattaatctcgttattagtttgattgacttgtcttt
atccttatacttttaagaaagattgacagtgggtgctgactactgccacatgccattaaacgggagtggttaaacattaaaagtaatacatgaggctaattcctttcatttag
aataaggaaagtgttttctataatgaataatgccgcactaatgcaaaaagacgaagattatcttaacaagggggattaagcataccgaaggaaaagagagtaatat
accagtggttgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaatttggtagccgaatttggtaaaagcccagggttatccatggtggccg
gccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcatttaattgtcttatataaggtttgggttttttctgacttcaatttgcattgggtgaaaagaaata
gtgtaagccattattggattccgaaatagccaaatttctgggttctcaaaagcgggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcctcctgatttaaggag
gaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgcaaaaagaaaatacattgggagacatcttctgatgaatcagatgcgga
gagtatctccagcggaatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgttcgacttctcgtagctctacgcagtaagtaccaaagggtacc

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FIGURE 31

EST2 pep	FFYCTEISST VTIVYFRHDT WN----KLIT F-----FIVE YFK-TYLVEN	40
Euplotes pep	FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSCLTI VKVRIQFSEK NKQMKNNFYQ	44
Consensus	FFY.TE..K. .S..YYRK. IW...-KL.. -----F..KV..	50
EST2 pep	NVCRNHNSY- ----- TLSNFNHNSK- RUTPKKGNNE FRUITAIPCRG	79
Euplotes pep	KEVEEWKKS- ----- --GFAPCK- RUTPKKIT-- FRFIMTFNKK	78
Trans of tetrahymen	KIQLEENLE KVEEKLIPED SFQKYPQCK- RUTPKKGS-- FRFIMTFLRK	92
Consensus	K...E..... -----F..GKE- RUTPKK...-- FRFIMTF.RK	100
EST2 pep	ADEEEFTIYK ENHKNAIQPT OKILEYLRNK RPTSFTKIYS PTQIADRIKE	129
Euplotes pep	IVNSDRKTTK LTNTKLLNS- HLMKTKLN- -----RMFK -DPFGFAVFN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS- QLVFRNEKD- -----ML-G -QKIGYSVFD	130
ConsensusK..K LN.N..L..S-QL..L..LKN- -----...-..IG..VF.	150
EST2 pep	FKQRLKKFN NVL----- FEFYFMKFD VKSCYD	157
Euplotes pep	YD-DVMKKE EFVCKWKQVG QKKEFFATMD IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWKNGK RFEYAYVTL- -----	158
Consensus	.K-...KFF. .F..KWK..G .E..LYF.T.D ...CYD	186

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

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FIGURE 33

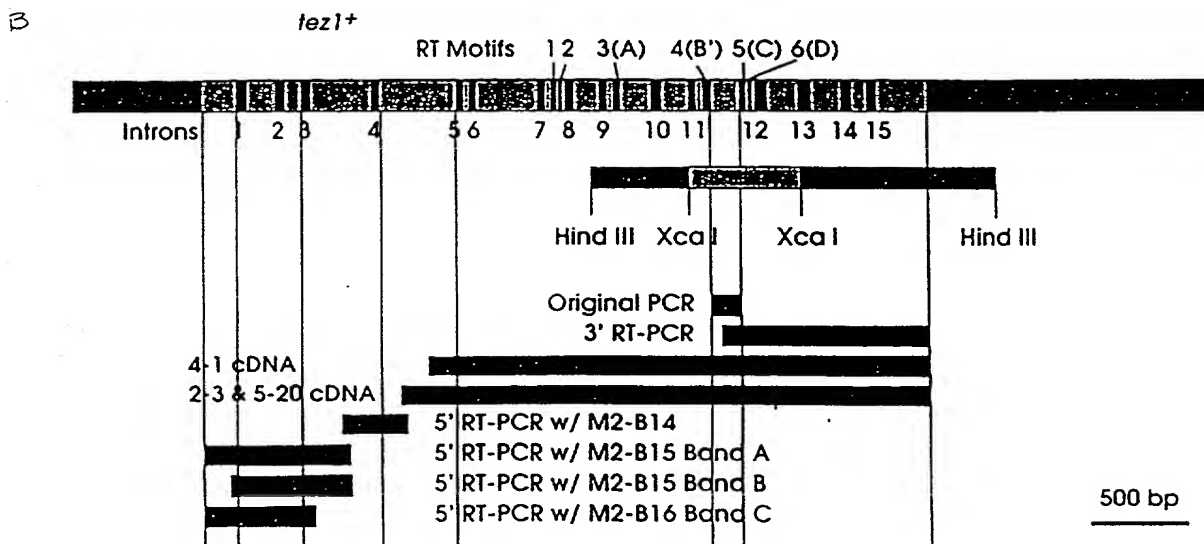
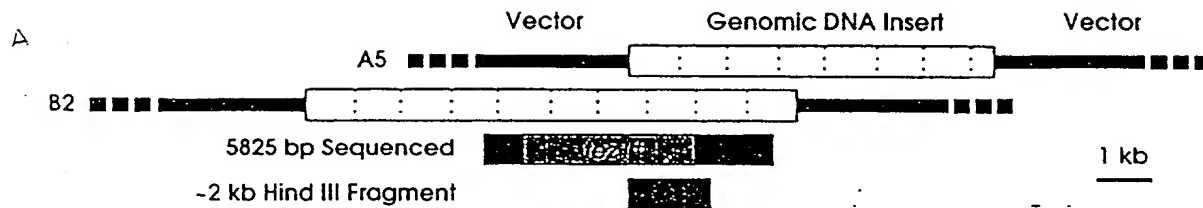


FIGURE 34

Poly 4

			t		t		c		
	t	a	a	g	c	c	t	c	g
5'-	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

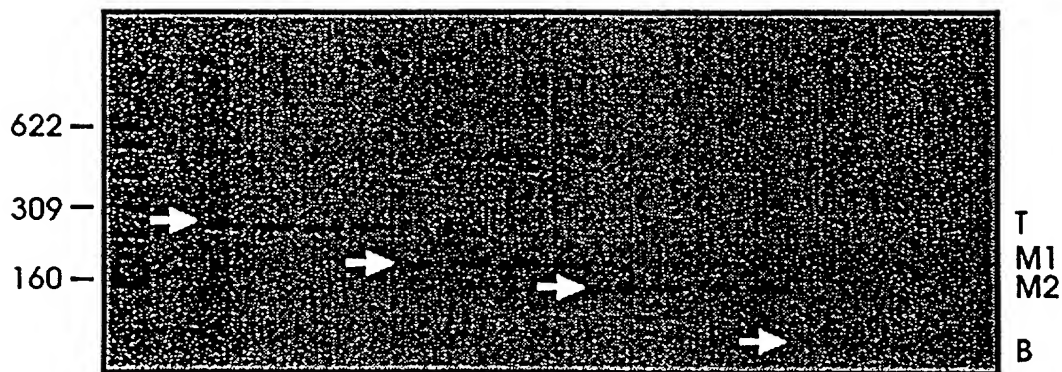
4 (B')

5 (C')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
				t	t	t	t	
						c	c	

Poly 1

FIGURE 35



Motif B' (4)
QTKGIPQG

Motif C (5)
DDYLLIT

208770.1.2.4.501

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

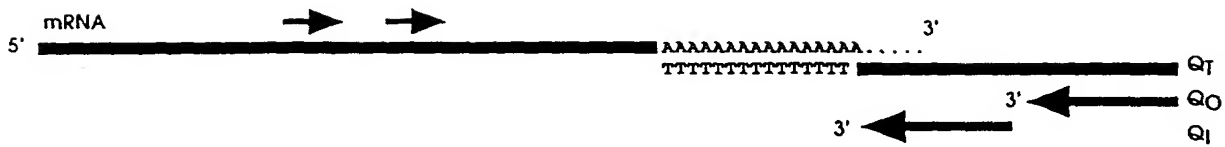
```

.....gac gat ttc ctc ttt ata aca.....  <---Actual Genomic Sequence.
      D  D  F  L  F  I  T

```

FIGURE 37

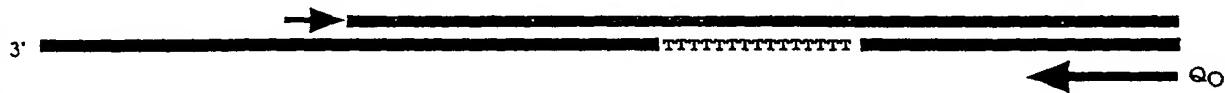
3' RT PCR Strategy



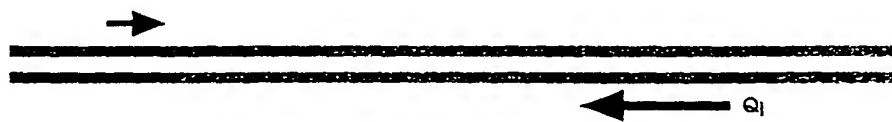
1. Synthesis of cDNA with QT Primer.



2. First Round PCR Using Outside Primer and QO Primer.



3. Second Round PCR Using Inside Primer and QI Primer.



4. Sequence Second Round PCR Products Using Inside Primer or QI Primer.

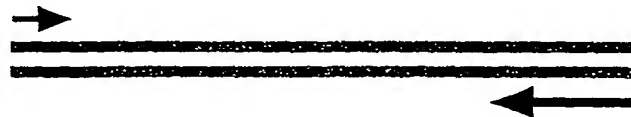


FIGURE 38

A

-Size Selected Libraries from P. Nurese

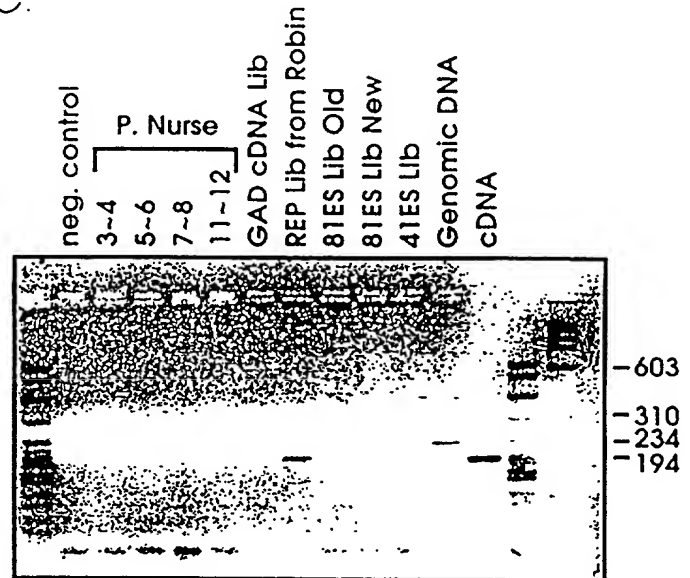
3 ~ 4 kb
5 ~ 6 kb
7 ~ 8 kb
11 ~ 12 kb

-Libraries from J.A. Wise
Sau 3a Partial Digest
Hind III Partial Digest

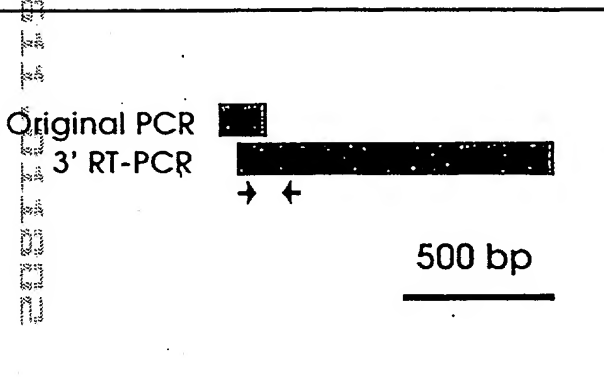
cDNA Libraries

GAD (Gal Activation Domain) Library
REP Library from R. Allshire
REP81ES Library (old)
REP81ES Library (new)
REP41ES Library

C



B



D

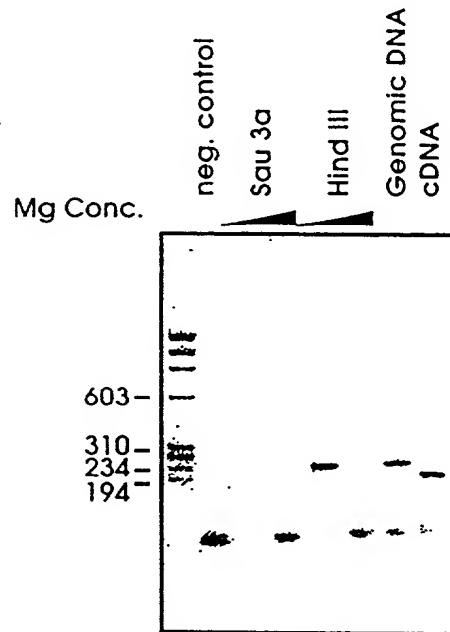
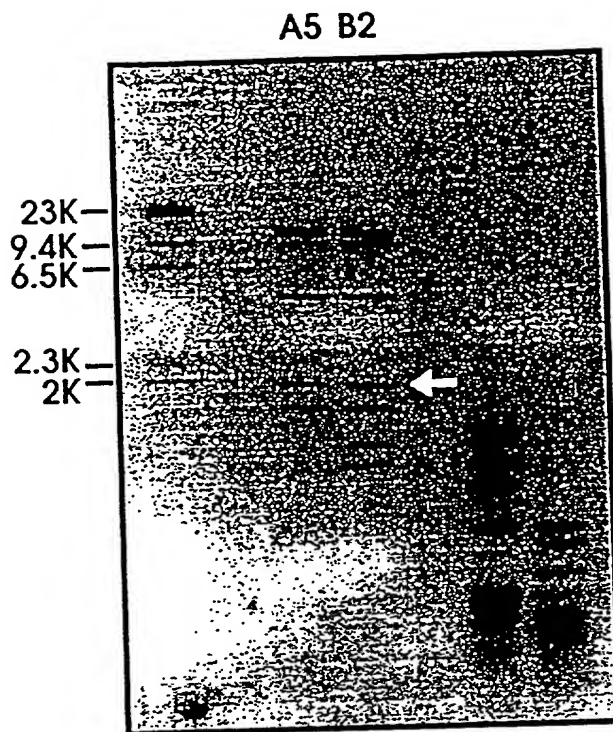


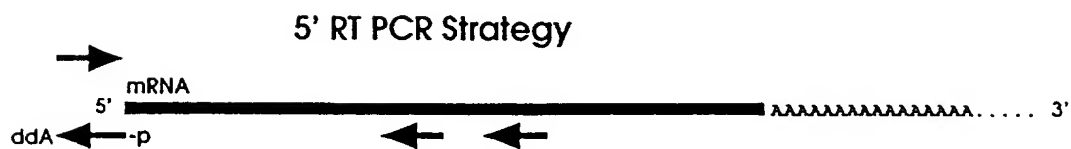
FIGURE 39



Hind III Digested Positive Genomic Clones

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FIGURE 40



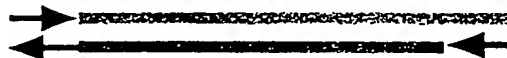
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

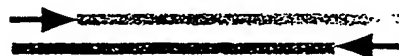


FIGURE 42

A

Sp_Tp1p :MTEHNTPKSRILRFLENOYVYLCT 24
Sc_Ea2p :MKLFEF 24
Ea_p123 : MEVDVOMQADNHQINSALKTCCEIEKEANT YSW 24

Sp_Tp1p : LNDYVOLYLRGSPA S SWICERLRSDVOTSF 31
Sc_Ea2p : IOKKLDIDLOTH T K ENIKCKGMFLGD 31
Ea_p123 : IOKVIRCRNOSO M K DLEDIKIFAOTN 31

Sp_Tp1p : IFLNSTYVGFDSKPDQVGFSSPKCSQSEL 47
Sc_Ea2p : EILTTCFALPMSR KIALPCPLGDLSSKAY 47
Ea_p123 : IVATPROYNEEDFKVIRKEVYFSTGLMILDK 47

Sp_Tp1p : VVKOMFDEBFERR HLLMK FSNMHEDFRAMH 127
Sc_Ea2p : CIIYLLTQELYN HVLTP FOLKARNED 127
Ea_p123 : CLVELLSDDVSDROKLOCC FOLKQNO 127

Sp_Tp1p : VNGVOMOLYSTFPNYLISILESKA OLLEI 154
Sc_Ea2p : YNMSLFCMSAHMYVTLKGAAL KMFNSLY 154
Ea_p123 : LAKTHLLTALSTOKYFFODE NOYRAM 154

Sp_Tp1p : SDAMHY LSKGS IFEALPNHNL IS IPLFKN 164
Sc_Ea2p : TYAFVD LINTYVIOFN GOFFT IY WRNCEP 164
Ea_p123 : NELFRNHTYKLI FORTSEOTLY FCMHNVFDM 164

Sp_Tp1p : NVFEETSKKRTIETSIION K SARKE 214
Sc_Ea2p : HLPFKWVO R SSSSATAAGI KOLTER 214
Ea_p123 : LKYNDFDK KOKGGAOMNEPRCCSTCKYNK 214

Sp_Tp1p : WNSISIRFSIFYRSYK KODYFLNLSCD 224
Sc_Ea2p : KILPSS SIKKTLKRLAEFF 224
Ea_p123 : NEK DNFLNNINYPNWHNSRTFFCTN 224

Sp_Tp1p : RNTYHMLWLOW IFPROGLINAFQYKOLNHYIPL 264
Sc_Ea2p : R SIKKTLKRLAEFF 264
Ea_p123 : R NHOFFKKEFYVSKNNISANDRAOT 264

Sp_Tp1p : VS OSTVYPKLLKYVPLEQOTAKRLNHS 313
Sc_Ea2p : TH LVKIPORLEKVINHLTLOKLRKRLN 313
Ea_p123 : FTHIFRFRNIRKELKDEKIEKATVLEKQDFN 313

Sp_Tp1p : LSKVYNNY YID THODEKISYSLKPN 347
Sc_Ea2p : YVSLNLSI PLEQVTLDLHLSNOSPKE 347
Ea_p123 : FHYLTYSI LPEWRERKOKIELINKTREEK 347

Sp_Tp1p : FA LRSILVRYV KLI 360
Sc_Ea2p : LK IIVLOKLL ODM 360
Ea_p123 : SKYEEELFSTYTONKCTO INEFFYNI KOF 360

Sp_Tp1p : WGNORIFEIIL DLETFK LRYESFSLMY 369
Sc_Ea2p : FGSKKNGKII LMLNLS PLNGYLPFDS 369
Ea_p123 : LTG ANRKNFO KYKKYVEKHELINHL 369

Sp_Tp1p : NIKISEIL LVLOKRSNAKMLCSO KKKOIFA 423
Sc_Ea2p : KRLKDF LFIS DIWFTKNNF LNLNLA 423
Ea_p123 : KINTREISMOVETS AKNFYVFOH N IYVLW 423

Sp_Tp1p : EFIV LYSNFIPILOS C SSDLNRTV 454
Sc_Ea2p : CFIS LFDOLIPKIIOT C ISSSTYV IV 454
Ea_p123 : KLLR IFEDLVSLIRC C OOKSYKMY 454

Sp_Tp1p : FKDI KLLCRPP ISMMEAEKINENHNRMD 467
Sc_Ea2p : FKDI KLLCRPP VETFKTLVNNYNNHNS 467
Ea_p123 : YKNI DVINKMSADLEKETLAEVQEKVEEW 467

Sp_Tp1p : TOKTTLPPAVI LL NTLKRL 502
Sc_Ea2p : VHLSSKRLKRLAEFF 502
Ea_p123 : KKSLOFAPKLL NTLKRLAEFF 502

Sp_Tp1p : KKSLOFAPKLL NTLKRLAEFF 502
Sc_Ea2p : KKSLOFAPKLL NTLKRLAEFF 502
Ea_p123 : KKSLOFAPKLL NTLKRLAEFF 502

Sp_Tp1p : ESSOIFPHLEVYMKLLTFKKOLL HRMFOR K 567
Sc_Ea2p : SFTKIYSPTOIADRIKEKORLL KPNHVLPE 567
Ea_p123 : KDPFGAFYFNDYVMEKYEFCV KWOYGOPEL 567

Sp_Tp1p : YVRI IKS RIKODLFRIV KKLKDE 614
Sc_Ea2p : YMKF VKS SIPRMECHRL DALKHNSC 614
Ea_p123 : FIATM IER SVHREKLSFL TTKLLSSD 614

Sp_Tp1p : VIRKATINATSDRATKN 620
Sc_Ea2p : FVRSOYFFNTHTG 620
Ea_p123 : WMTAOLKRNHNIYDSEKFRKKEKMYDFOK 620

Sp_Tp1p : FYSEAFSYFONVPEK LOLS MKTSO 654
Sc_Ea2p : VSKSFFYFONVPEK LOLS MKTSO 654
Ea_p123 : NOKILEGOOYPTLS LENEONOLNAKKT 654

Sp_Tp1p : FQYWTSSSEIFKMKENLSOHVYKIONSO 667
Sc_Ea2p : DHVRTYHLSHODYINVVEHIFKHALWYEDKC 667
Ea_p123 : EAKORNTYFKDNLLOPVINICQYNTYINFGK 667

Sp_Tp1p : LOKV IPI SIL SPCLHYMED IDEYLS 721
Sc_Ea2p : IRED LPSILSAP IYDLYVDD LEYSSEKA 721
Ea_p123 : KOTK IPI LCV SILSSFYAT LESSLGLR 721

Sp_Tp1p : KKG SYLLRYV F FVYVKKDAKK 726
Sc_Ea2p : SP5OD TLILKLL TIBYDGOOYIN 726
Ea_p123 : DESMPEPHVHLLMLR YLLTTOENNAVY 726

Sp_Tp1p : FLNLSLQFKEKNHSTSL YVINEN NG 766
Sc_Ea2p : IKKLAGOPKYNHAKAND ILAYSSO D 766
Ea_p123 : FIEKLINVSRENQFPMKLOTSPLEPSKFA 766

Sp_Tp1p : IINNTHFFNESKKRPF FVHNRSDTL 814
Sc_Ea2p : DDTVIOFCA WHIFKELEVWKSSTM 814
Ea_p123 : KYGMSVEEONIVODYCDWIGISIDMKLALMP 814

Sp_Tp1p : ACCK IDEALFNSTSVELTKHMGKSFY ILS 867
Sc_Ea2p : NFNHRSKSKOIFRSLIANTRISTY TIDTH 867
Ea_p123 : HINLRIGILCTLHLMNMOGKASMWLKLKFS 867

Sp_Tp1p : ASFAQVDFIDITHNSKFSCCN IYALGYSNCR 902
Sc_Ea2p : NSTNTVLMODHNVYKNISEC 902
Ea_p123 : MNNITHYFRKTITTEDFANKTLNKFISGOYK 902

Sp_Tp1p : AGAYLKNR IFIPORMFITOLLNVIOKWK 913
Sc_Ea2p : YKSAP LSLIN YTHOMHNSFOR 913
Ea_p123 : YMOCAKET MFKKNLANSNIDLEYSKI YSY 913

Sp_Tp1p : LAEILQYTSRRFLSSAEYKWLFCLOMROG 954
Sc_Ea2p : YSOCPKLP IYERFFTLILHES 954
Ea_p123 : NAFKFLVYHIKOTIFGEENYPOFSLH 954

Sp_Tp1p : FKYNPCFEOLYOSLTDILKPLRPV ROYLF 961
Sc_Ea2p : TS KKNHILKKEIOM GAYIY 961
Ea_p123 : IEIFS TKKVIHNYCHILAKKAKESOC 961

Sp_Tp1p : LNRRIAD 966
Sc_Ea2p : IYINIVH 966
Ea_p123 : OSLIOYDA 966

B

Sp_Tp1p :MTEHNTPKSRILRFLENOYVYLCT 24
Sc_Ea2p :MKLFEF 24
Ea_p123 : MEVDVOMQADNHQINSALKTCCEIEKEANT YSW 24

Sp_Tp1p : LNDYVOLYLRGSPA S SWICERLRSDVOTSF 31
Sc_Ea2p : IOKKLDIDLOTH T K ENIKCKGMFLGD 31
Ea_p123 : IOKVIRCRNOSO M K DLEDIKIFAOTN 31

Sp_Tp1p : IFLNSTYVGFDSKPDQVGFSSPKCSQSEL 47
Sc_Ea2p : EILTTCFALPMSR KIALPCPLGDLSSKAY 47
Ea_p123 : IVATPROYNEEDFKVIRKEVYFSTGLMILDK 47

Sp_Tp1p : VVKOMFDEBFERR HLLMK FSNMHEDFRAMH 127
Sc_Ea2p : CIIYLLTQELYN HVLTP FOLKARNED 127
Ea_p123 : CLVELLSDDVSDROKLOCC FOLKQNO 127

Sp_Tp1p : VNGVOMOLYSTFPNYLISILESKA OLLEI 154
Sc_Ea2p : YNMSLFCMSAHMYVTLKGAAL KMFNSLY 154
Ea_p123 : LAKTHLLTALSTOKYFFODE NOYRAM 154

Sp_Tp1p : SDAMHY LSKGS IFEALPNHNL IS IPLFKN 164
Sc_Ea2p : TYAFVD LINTYVIOFN GOFFT IY WRNCEP 164
Ea_p123 : NELFRNHTYKLI FORTSEOTLY FCMHNVFDM 164

Sp_Tp1p : NVFEETSKKRTIETSIION K SARKE 214
Sc_Ea2p : HLPFKWVO R SSSSATAAGI KOLTER 214
Ea_p123 : LKYNDFDK KOKGGAOMNEPRCCSTCKYNK 214

Sp_Tp1p : WNSISIRFSIFYRSYK KODYFLNLSCD 224
Sc_Ea2p : KILPSS SIKKTLKRLAEFF 224
Ea_p123 : NEK DNFLNNINYPNWHNSRTFFCTN 224

Sp_Tp1p : RNTYHMLWLOW IFPROGLINAFQYKOLNHYIPL 264
Sc_Ea2p : R SIKKTLKRLAEFF 264
Ea_p123 : R NHOFFKKEFYVSKNNISANDRAOT 264

Sp_Tp1p : VS OSTVYPKLLKYVPLEQOTAKRLNHS 313
Sc_Ea2p : TH LVKIPORLEKVINHLTLOKLRKRLN 313
Ea_p123 : FTHIFRFRNIRKELKDEKIEKATVLEKQDFN 313

Sp_Tp1p : LSKVYNNY YID THODEKISYSLKPN 347
Sc_Ea2p : YVSLNLSI PLEQVTLDLHLSNOSPKE 347
Ea_p123 : FHYLTYSI LPEWRERKOKIELINKTREEK 347

Sp_Tp1p : FA LRSILVRYV KLI 360
Sc_Ea2p : LK IIVLOKLL ODM 360
Ea_p123 : SKYEEELFSTYTONKCTO INEFFYNI KOF 360

Sp_Tp1p : WGNORIFEIIL DLETFK LRYESFSLMY 369
Sc_Ea2p : FGSKKNGKII LMLNLS PLNGYLPFDS 369
Ea_p123 : LTG ANRKNFO KYKKYVEKHELINHL 369

Sp_Tp1p : NIKISEIL LVLOKRSNAKMLCSO KKKOIFA 423
Sc_Ea2p : KRLKDF LFIS DIWFTKNNF LNLNLA 423
Ea_p123 : KINTREISMOVETS AKNFYVFOH N IYVLW 423

Sp_Tp1p : EFIV LYSNFIPILOS C SSDLNRTV 454
Sc_Ea2p : CFIS LFDOLIPKIIOT C ISSSTYV IV 454
Ea_p123 : KLLR IFEDLVSLIRC C OOKSYKMY 454

Sp_Tp1p : FKDI KLLCRPP ISMMEAEKINENHNRMD 467
Sc_Ea2p : FKDI KLLCRPP VETFKTLVNNYNNHNS 467
Ea_p123 : YKNI DVINKMSADLEKETLAEVQEKVEEW 467

Sp_Tp1p : TOKTTLPPAVI LL NTLKRL 502
Sc_Ea2p : VHLSSKRLKRLAEFF 502
Ea_p123 : KKSLOFAPKLL NTLKRLAEFF 502

Sp_Tp1p : KKSLOFAPKLL NTLKRLAEFF 502
Sc_Ea2p : KKSLOFAPKLL NTLKRLAEFF 502
Ea_p123 : KKSLOFAPKLL NTLKRLAEFF 502

Sp_Tp1p : ESSOIFPHLEVYMKLLTFKKOLL HRMFOR K 567
Sc_Ea2p : SFTKIYSPTOIADRIKEKORLL KPNHVLPE 567
Ea_p123 : KDPFGAFYFNDYVMEKYEFCV KWOYGOPEL 567

Sp_Tp1p : YVRI IKS RIKODLFRIV KKLKDE 614
Sc_Ea2p : YMKF VKS SIPRMECHRL DALKHNSC 614
Ea_p123 : FIATM IER SVHREKLSFL TTKLLSSD 614

Sp_Tp1p : VIRKATINATSDRATKN 620
Sc_Ea2p : FVRSOYFFNTHTG 620
Ea_p123 : WMTAOLKRNHNIYDSEKFRKKEKMYDFOK 620

Sp_Tp1p : FYSEAFSYFONVPEK LOLS MKTSO 654
Sc_Ea2p : VSKSFFYFONVPEK LOLS MKTSO 654
Ea_p123 : NOKILEGOOYPTLS LENEONOLNAKKT 654

Sp_Tp1p : FQYWTSSSEIFKMKENLSOHVYKIONSO 667
Sc_Ea2p : DHVRTYHLSHODYINVVEHIFKHALWYEDKC 667
Ea_p123 : EAKORNTYFKDNLLOPVINICQYNTYINFGK 667

Sp_Tp1p : LOKV IPI SIL SPCLHYMED IDEYLS 721
Sc_Ea2p : IRED LPSILSAP IYDLYVDD LEYSSEKA 721
Ea_p123 : KOTK IPI LCV SILSSFYAT LESSLGLR 721

Sp_Tp1p : KKG SYLLRYV F FVYVKKDAKK 726
Sc_Ea2p : SP5OD TLILKLL TIBYDGOOYIN 726
Ea_p123 : DESMPEPHVHLLMLR YLLTTOENNAVY 726

Sp_Tp1p : FLNLSLQFKEKNHSTSL YVINEN NG 766
Sc_Ea2p : IKKLAGOPKYNHAKAND ILAYSSO D 766
Ea_p123 : FIEKLINVSRENQFPMKLOTSPLEPSKFA 766

Sp_Tp1p : IINNTHFFNESKKRPF FVHNRSDTL 814
Sc_Ea2p : DDTVIOFCA WHIFKELEVWKSSTM 814
Ea_p123 : KYGMSVEEONIVODYCDWIGISIDMKLALMP 814

Sp_Tp1p : ACCK IDEALFNSTSVELTKHMGKSFY ILS 867
Sc_Ea2p : NFNHRSKSKOIFRSLIANTRISTY TIDTH 867
Ea_p123 : HINLRIGILCTLHLMNMOGKASMWLKLKFS 867

Sp_Tp1p : ASFAQVDFIDITHNSKFSCCN IYALGYSNCR 902
Sc_Ea2p : NSTNTVLMODHNVYKNISEC 902
Ea_p123 : MNNITHYFRKTITTEDFANKTLNKFISGOYK 902

Sp_Tp1p : AGAYLKNR IFIPORMFITOLLNVIOKWK 913
Sc_Ea2p : YKSAP LSLIN YTHOMHNSFOR 913
Ea_p123 : YMOCAKET MFKKNLANSNIDLEYSKI YSY 913

Sp_Tp1p : LAEILQYTSRRFLSSAEYKWLFCLOMROG 954
Sc_Ea2p : YSOCPKLP IYERFFTLILHES 954
Ea_p123 : NAFKFLVYHIKOTIFGEENYPOFSLH 954

Sp_Tp1p : FKYNPCFEOLYOSLTDILKPLRPV ROYLF 961
Sc_Ea2p : TS KKNHILKKEIOM GAYIY 961
Ea_p123 : IEIFS TKKVIHNYCHILAKKAKESOC 961

Sp_Tp1p : LNRRIAD 966
Sc_Ea2p : IYINIVH 966
Ea_p123 : OSLIOYDA 966

FIGURE 43

Disruption strategy for the putative telomerase genes.

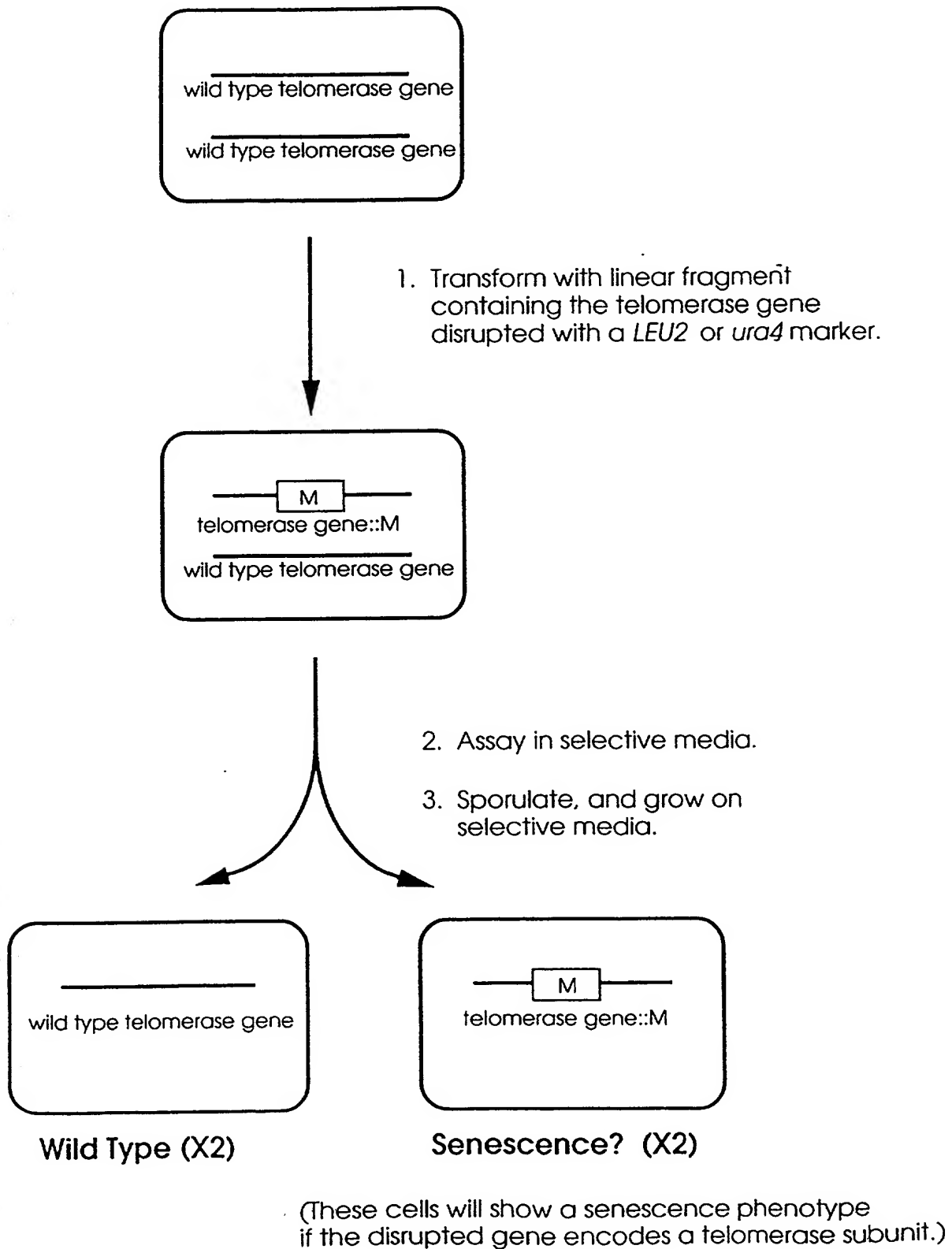


FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

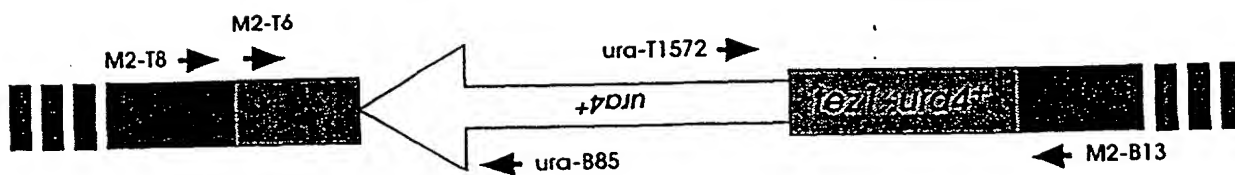
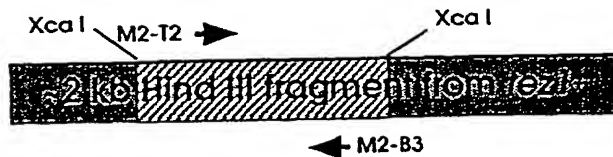
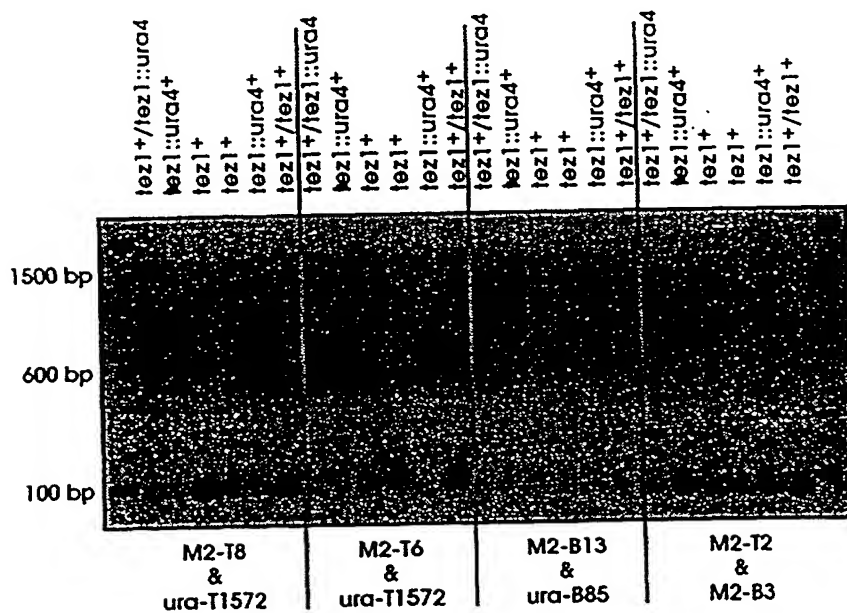


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

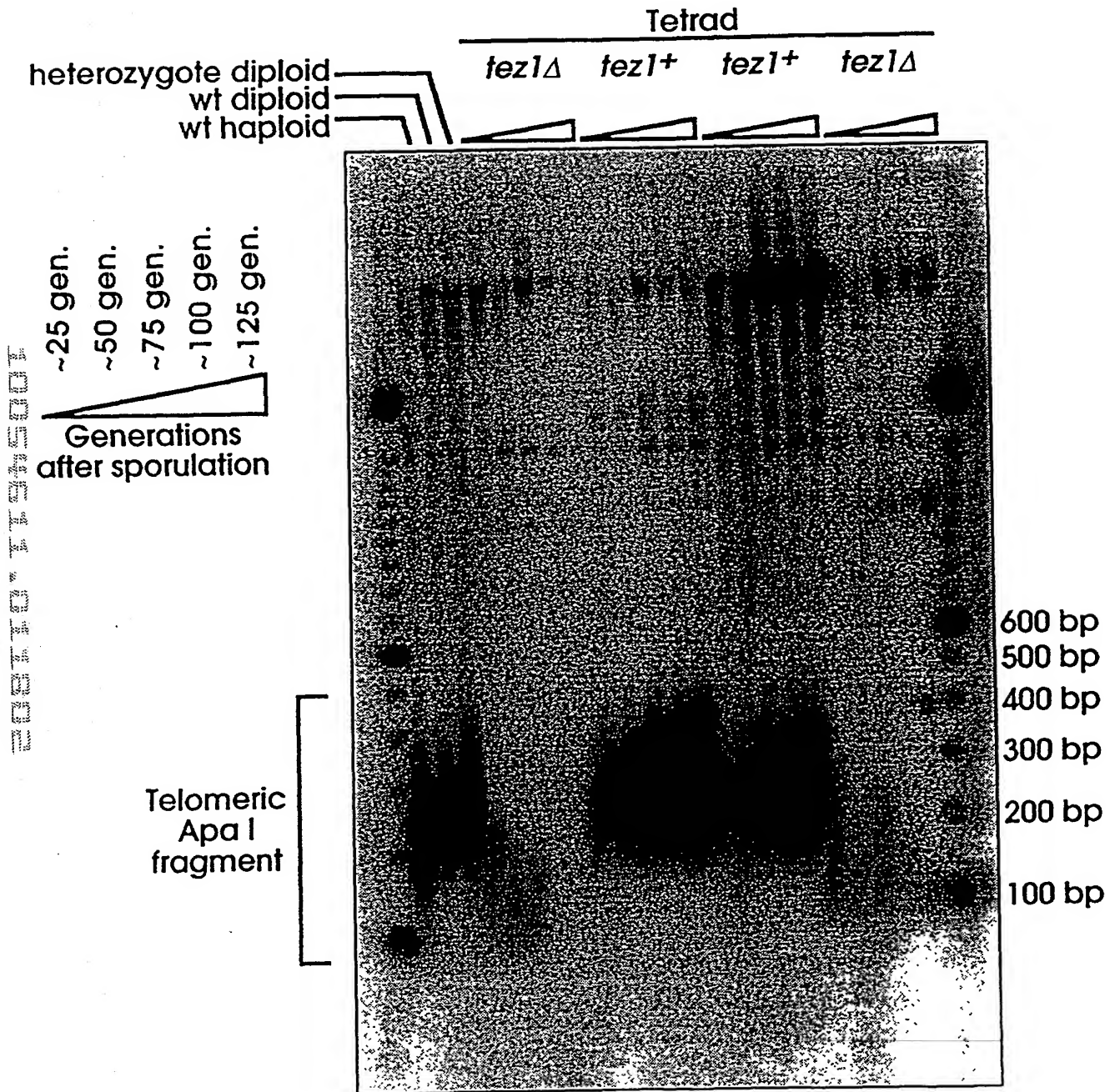


FIGURE 46

1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataatatttctattttatcgggtcggtta 160
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240
241 gggtcgcttacttttaatcgtggtagtctgttttagctgctacttctagccaaccgctgtttctaccccgctcattggatat 320
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcctgcatattc 400
401 ttaacatggagccttacacttttagatgagtcacgtcgcgatgaggagtatttggtatcatccaacgtttgcttgaaaag 480
481 gttgataattatttgcaaaatcatgtccttagtgggtggaatccgcgaaagttttttgatgcttgacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctatttctcatgttggt 640
641 ccaaatatgtatcatctcgtatttaggttttttccggttttactcctggaatcgtaacctttttcactattccccctaataga 720
721 ataactctaaattagtttcgcttataattgatagtagtagaaaagattgggtgattctactcgtgtaatgttattagtttaa 800
801 gatacttttgcaaaacatttatttagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
881 actattttattttaaacggttatgatcagtaggacactttgcatatatatagttatgcttaatgggttacttgtaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

1199	AAA TGC TCA CAG TCA GAG gtatatatatattttgttttgatttttttctattcgggatagctaatatatgggcag	1272
81	K C S Q S E	86
1273	CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA	1332
87	L I A N V V K Q M F D E S F E R R R N L	106
1333	CTG ATG AAA GGG TTT TCC ATG gtaaggtatttctaattgtgaaatattttacctgcaattactgttttcaaagaga	1405
107	L M K G F S M	113
1406	ttgtattttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114	N H E D F R A M H V N G V Q N	128
1470	GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529
129	D L V S T F P N Y L I S I L E S K N W Q	148
1530	CTT TTG TTA GAA AT gtaaataaccggtaagatgttgcgactttgaacaagactgacaagtatag T ATC GGC	1601
149	L L L E I I G	155
1602	AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC	1661
156	S D A M H Y L L S K G S I F E A L P N D	175
1662	AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG	1721
176	N Y L Q I S G I P L F K N N V F E E T V	195
1722	TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA	1781
196	S K K R K R T I E T S I T Q N K S A R K	215
1782	GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841
216	E V S W N S I S I S R F S I F Y R S S Y	235
1842	AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaatttttag AT CTA TAT TTT AAC	
1907		
236	K K F K Q D L Y F N	245
1908	TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967
246	L H S I C D R N T V H M W L Q W I F P R	265
1968	CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA	2027
266	Q F G L I N A F Q V K Q L H K V I P L V	285
2028	TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA	2087
286	S Q S T V V P K R L L K V Y P L I E Q T	305
2088	GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT	2147
306	A K R L H R I S L S K V Y N H Y C P Y I	325
2148	GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG	2207
326	D T H D D E K I L S Y S L K P N Q V F A	345
2208	TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA	2267
346	F L R S I L V R V F P K L I W G N Q R I	365
2268	TTT GAG ATA ATA TTA AAA G gtattgtataaaaattttattaccactaacgattttaccag AC CTC GAA ACT	2336
366	F E I I L K D L E T	375

FIGURE 46 (cont.)

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396	
376	F L K L S R Y E S F S L H Y L M S N I K	395	
2397	gtaatatgccaaatttttttaccattaattaacaatcag	ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396		I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525	
406	K R S N A K M C L S D F E K R K Q I F A	425	
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585	
426	E F I Y W L Y N S F I I P I L Q S F F Y	445	
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645	
446	I T E S S D L R N R T V Y F R K D I W K	465	
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705	
466	L L C R P F I T S M K M E A F E K I N E	485	
2706	gtatttttaaagtatttttttgcaaaaagctaatttttcag	AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486		N N V R M D T Q K T	495
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835	
496	T L P P A V I R L L P K K N T F R L I T	515	
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaattctatta	2906	
516	N L R K R F L I K	524	
2907	ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967	
525	M G S N K K M L V S T N Q T L R P V	542	
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027	
543	A S I L K H L I N E E S S G I P F N L E	562	
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088	
563	V Y M K L L T F K K D L L K H R M F G	581	
3089	tatataatgcgcgattcctcattattaattttgcag	G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA	3155
582		R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215	
592	K S C Y D R I K Q D L M F R I V K K K L	611	
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275	
612	K D P E F V I R K Y A T I H A T S D R A	631	
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaattttttaacaa	3343	
632	T K N F V S E A F S Y F	643	
3344	attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405	
644		D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465	
660	S D T L F V D F V D Y W T K S S S E I F	679	
3466	AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca	3532	
680	K M L K E H L S G H I V K	692	

3533	ctaataaaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	3593
693	I G N S Q Y L Q K V G I P Q G S	708	
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtagattgtctgcatcc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	taagtcttaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840	
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG	4089	
839	K S F F Y K I L R	S 848	
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtagtactttttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC	4339	
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	ggctctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA	4468	
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q S L T	966	
4529	GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA tgtcattttcaatttattatatatacatcctttattactgggtgtcttaaacaatattattactaagtata	4665	
987	A D *	989	



4666	gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct	4745
4746	ttatccttatacttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca	4825
4826	ttaaaagtaatacatgaggctaatactccttttcatttagaataaggaaagtggttttctataatgaataatgccgcacta	4905
4906	atgcaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaatataccagtggt	4985
4986	gttgaagaaagcaaggataatttggacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc	5065
5066	cccagggttatccatggtggccggccttgctactgagacgaaaagaaactaaggtagtltgaatactaatagctcattta	5145
5146	atgtcttatataagggttttgttttttctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat	5225
5226	tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc	5305
5306	tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc	5385
5386	aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata	5465
5466	acttctattttctgaaatgtatggtcctactgtcgccttcgacttctcgtagctctacgcagttaagtgaccaaagggtacc	5544

[illegible]

FIGURE 47

[illegible]

FIGURE 47 (cont.)

190	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	200	gln	lys	ala	ala	met										
	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC		CAG	AAG	GCC	GCC	ATG										
											210	gly	thr	ser	ala	arg	pro	ser	arg	ala	thr	ser	tyr	val	gln	cys
												GGC	ACG	TCC	GCA	AGG	CCT	TCA	AGA	GCC	ACG	TCC	TAC	GTC	CAG	TGC
220	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	230	thr	leu	leu	cys	ser										
	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC		ACG	CTG	CTC	TGC	AGC										
											240	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	ile	arg
												CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG
250	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	260	asp	phe	leu	leu	val										
	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT		GAT	TTC	TTG	TTG	GTG										
											270	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	leu	val
												ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	CTG	GTC
280	arg	gly	val	pro	glu	tyr	gly	cys	val	val	290	asn	leu	arg	lys	thr										
	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG		AAC	TTG	CGG	AAG	ACA										
											300	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	thr	ala
												GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	ACG	GCT
310	phe	val	gln	met	pro	ala	his	gly	leu	phe	320	pro	trp	cys	gly	leu										
	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC		CCC	TGG	TGC	GGC	CTG										
											330	leu	leu	asp	thr	arg	thr	leu	glu	val	gln	ser	asp	tyr	ser	ser
												CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	TAC	TCC	AGC
340	tyr	ala	arg	thr	ser	ile	arg	ala	ser	leu	350	thr	phe	asn	arg	gly										
	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC		ACC	TTC	AAC	CGC	GGC										
											360	phe	lys	ala	gly	arg	asn	met	arg	arg	lys	leu	phe	gly	val	leu
												TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	TTG
370	arg	leu	lys	cys	his	ser	leu	phe	leu	asp	380	leu	gln	val	asn	ser										
	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT		TTG	CAG	GTG	AAC	AGC										

FIGURE 47 (cont.)

390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGT TTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTACCCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 48

Motif -1
Ep p123 ...LVVSLIRCFYVTEQQKSYSKT...
Sp Tez1 ...FIIPILQSFFYITESSDLNRNT...
Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1 ...YVVELLRSSFFYVTETTFQKNRL...
consensus FFY TE

Motif 0
Ep p123 ...KSLGFAPGKLRLLIPKKT--TFRPIMTFNKKIV...
Sp Tez1 ...QKTTLPFAVIRLLPCKN--TFRLLITNLRKRFL...
Sc Est2 ...TLNFFNHSMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus R PK R I

Motif A
Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus F D YD

Motif B
Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus G QG S

Motif C
Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
consensus DD L

Motif D
Ep p123 ...NVSRENGFKFNMKKL...
Sp Tez1 ...LNLSLRGFEEKHNFST...
Sc Est2 ...KKLAMGGFQKYNKA...
Hs TCP1 ...LRTLVRGVPEYGCVV...
consensus G

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FIGURE 49

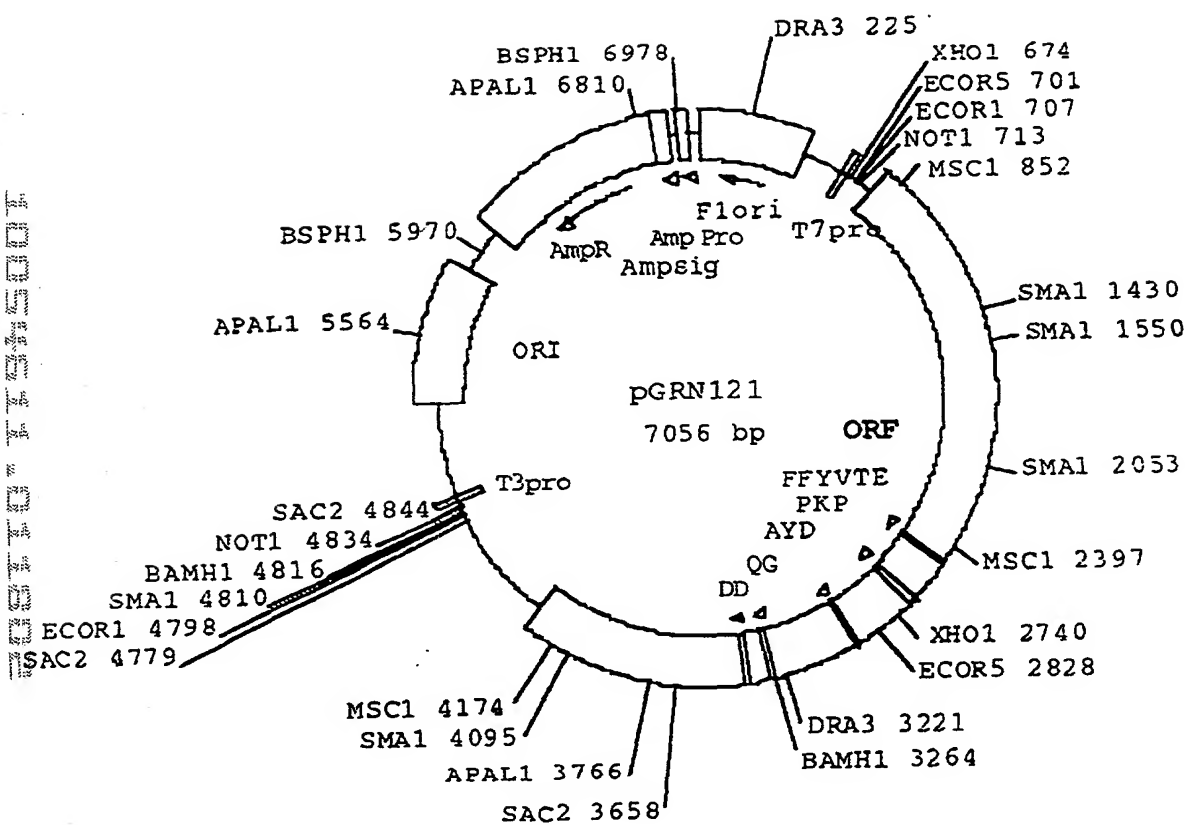


FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCCGCG GGGGCCCCC CGAGGCCTTC
 401 ACCACCAGCG TGCAGCTA CCTGCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGC GCGNTNT TTGTGCTGGT GGNTCCCAGC
 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCCGCCAC ACGTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCCG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCCTGG GCCACCCCG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTCCTCTAC
 1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTCCTACTC AATATATCTG
 1101 AGGCCAGCC TGAAGTGGT TCGGGAGGT CGTGGAGACA NTCTTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAAACCAG
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCTGCGC CGGCTGGTGC CCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TCGGGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
 1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTGCGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGCTTCA TCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCGCGAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTACGGA GGTCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTA CTGCTGCGT ATGCCGTGGT CCAGAAGGCC

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FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401 GCCCCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCCTTTGGT
2651 GGATGATTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801 GGCTTTTGT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGCGCTGC
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTT AACC GCGGCT TCAAGGCTGG
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA
3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGA GAACCCCA TTTTCTCTGC
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGCC CTCTGCCCTC
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCTGCTC AAGCTGACTC
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCCTCAG GACAGCCCAG
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401 CGCAGCCAAC CCGGCACTGC CTCAGACTT CAAGACCATC CTGGACTGAT
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801 GCCCTGCCCT CTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

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FIGURE 51

GCAGGCGTGGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGCCACCCCCCGGATGCC
 1 -----+-----+-----+-----+-----+ 60
 CTTCCCGACGCGAGGACGCGGTGCACCCCTTCGGGACCGGGGCCGGTGGGGGCGCTACCG
 a A A I R P A A H V G S P C P G H P R D A -
 b Q K C V L L R T W E A L A P A T P A M P -
 c S A A S C C A R G K P W F R P P F R C R -
 CCGGCTCCCTCGCTGCCGAGCCGTGGGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
 61 -----+-----+-----+-----+-----+ 120
 CCGCGAGAGGGCGAGCGCTCGGCACGCGAGGGACGAGCGGTGCGTGGCGCTCCACGA
 a A R S P L F S R A L P A A Q P L P R G A -
 b R A P R C R A V R S L L R S H Y R E V L -
 c A L P A A E P C A P C C A A T T A R C C -
 GCGGCTGGCCACGTTCTGTCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
 121 -----+-----+-----+-----+-----+ 180
 CGCGGACCGGTGCAAGCACGCCCGCGGACCCCGGGTCCCGACCGCCGACCACGTCCGCTC
 a A A G H V R A A P G A P G I A A G A A R -
 b P L A T F V R R L G P Q G W R L V Q R G -
 c R W P R S C G A W G P R A C G W C S A G -
 GGACCGCGCGCTTTCCCGCGGNTGGTGGCCANTGCTGCTGCTGCGCTGGGANGN
 181 -----+-----+-----+-----+-----+ 240
 CCTGGGCGCGCGAAAGGCGCGGNACCACCGGGTNACGNACCACACGCGCGCACCCCTNKN
 a G P G G F P R ? G G P ? ? G V R A L G ? -
 b D P A A F R A ? V A ? C ? V C V P W ? ? -
 c T R R L S A R W W P ? A W C A C P G ? ? -
 ANGGLNGCCCCCGCGCGCCCCCTCCCTCCCGCCAGGTGCTCTGCTGAANGANCTGGTGGC
 241 -----+-----+-----+-----+-----+ 300
 TNCCGNCGCGCGCGCGCGGGGAGGAAGCGGTCCACAGGACCGACTTNCINGACCAACG
 a ? A A F R R P L L P P G V L P E ? ? G G -
 b ? ? P P A A P S F R Q V S C L ? ? L V A -
 c G ? P P P P P P S A R C P A * ? ? W W P -
 CCGAGTCTGCANANGCTGTGCGANCCCCCGCGGAANAACGTGCTGGGCTTGGGCTTGGC
 301 -----+-----+-----+-----+-----+ 360
 GGCTCAGACGTNTNCGACACGCTNCGCGCGGCTTNTTSCACGACCGGAAGCCGAAGCG
 a P S A A ? A V R ? R R E ? R A G L R L R -
 b P V L ? ? L C ? R G A ? N V L A P C P A -
 c E C C ? ? C A ? A A R ? T C W P S A S R -
 GCTGCTGGAGCGGGCGCGGGGGCCCCCGGAGCCCTTTCACCACCGAGGTGGCGAGCTA
 361 -----+-----+-----+-----+-----+ 420
 CGACGACCTGCCCCGGGCGCGCCCCCGCGGCTTCGGGAAGTGGTGGTGCACCGCTGGAT
 a A A G R G P R G F P R G L H H Q R A Q L -
 b L L D G A R G G F P E A F T T S V R S Y
 c C W T G P A G A P F R P S P P A C A A T -

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FIGURE 51 (cont.)

421 CCTGCCCAACACGGTGAACGACGCACTGCGGGGAGCGGAGGCTGCTGCTGCG
-----+-----+-----+-----+ 480
CGACGGGTGTGCTCACTGGCTGCTGACGCGCTCTGCTCCGCAACCCCGAAGCAGGCG

a P A Q H G D R R T A G E F G V G A A A A -
b L P N T V T D A L R G S G A W G L L L K -
c C P T R * F T H C G G A G R G G C C C A -

491 CCGGCTGGGAGGAGCTGCTGGTTCACCTGCTGGCAGGCTGCGGCTNINITTCTCTGCT
-----+-----+-----+-----+ 540
GGCGCACCGGCTGCTGCAAGACCAAGTGGAGCAGCGTGGAGCGGCGNANAAACACGACCA

a P R C R R R A G S P A G T L R ? ? C A G -
b R V G D D V L V H L L A R C A ? F V L V -
c A W A T T C W F T C W H A A R ? L C W W -

541 GGNTCCCACTGCGGCTAACCANGTGTGCGGGCGCGGCTGTACCAAGCTCGGCGCTGCAAC
-----+-----+-----+-----+ 600
CCNAGGCTGACGCGGATGGTNCACACGCGCGCGGCGGACATGCTGAGCCCGGACGCTG

a G S Q L R L P ? V R A A A V P A R R C ? -
b ? P S C A Y ? V C G P P L Y Q L G A A T -
c ? P A A P T ? C A G R R C T S S A L ? L -

601 TCAGGCCCCGGCCCCCGCCACACCTANTGCAACCGAAGCGCTCTGGGATCCAAAGCGCT
-----+-----+-----+-----+ 660
AGTCGCGGCGCGGGCGGTGTGCGATNACCTGGGCTTNCGACAGCGCTAGTTGCGCGGA

a S C P A P A T R ? W T R ? R L G S N G P -
b Q A R P P P H A ? G P E ? V W D P T G L -
c R P G P R H T L ? D T ? A S G I Q R A W -

661 GGAACCATAGCGTCAAGGAGGCGCGGCTCCCCCTGCGCTCCCAACCCCGGCTCCGAGCAG
-----+-----+-----+-----+ 720
CCTTGTATGAGTCCCTCCGGCCCCAGGGGACCCCGACGGTCCGGGCCCCAGCTCCTC

a G T I A S C R P C S P W A A S P G C E E -
b E P * R Q G G R C P P G L P A F G A R R -
c N H S V R E A G V P L G C Q P R V R G G -

721 GCGCGGCCCCAGTCCAGCGCGAAGTCTGCGGTTGCCCAAGAAGCGCGGCTGGCGCTGC
-----+-----+-----+-----+ 780
CGGCGCCCCGCTCAGGTCGGCTTCAGACGGCAACGGGTTCCTCGGCTCCGACCGCGAAG

a A R G Q C Q P K S A V A Q E A Q A W R C
b R G G S A S R S L P L P K R P R R G A A
c A G A V F A E V C R C P R G P G V A L ? -

781 CCGTGAGCCCGAGCCGACCCCCCTTCCGACGGGTCCTGGGCCCCACCCGGGAGGAGCT
-----+-----+-----+-----+ 840
GGGACTGCGCTCTGCGGGCAACCGTCCCCAGGACCGGGTGGGCCCCCTCTGCGG

a P * A C A D A R W A C V L G F F G Q D A -
b P E P E R T P V G Q G S W A H P G R T P -
c L S R S G R P L G R G P G P T R A C R L -

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FIGURE 51 (cont.)

TGGACCGAGTGAACCGTGGTTCTGTGTGGTGTCACTCCACACCCGCCGAAGAAGCCAC
 841 -----+-----+-----+-----+-----+ 900
 ACCTGGCTCACTGGCACCAAGACACACCACAGTGGACGGTCTGGGGGCGCTTCTTCCGTG

a W T E * P W F L C G V T C Q T R R R S H -
 b G P S D R G F C V V S P A R P A E E A T
 c D R V T V V S V W C H L P D P P K K P F -

CTCTTTGGAGGGTGGCTCTCTGGCACGGGCGCTCCACCCATCCGTGGGCGCGACCA
 901 -----+-----+-----+-----+-----+ 960
 CAGAAACCTCCACCGGAGAGACCGTGGCGGTGAGGGTGGGTAGGCACCCGGCGGTCTGT

a L F G G C A L W H A P L P P I R G F F A
 b S L E G A L S G T R H S H P S V G R Q H -
 c L W R V R S L A R A T P T H P W A A S T -

CCAGCGGGGCGCCCATCCACATCGGGCCACCACGTCTTGGACACGGCTTGTTCCTCCG
 961 -----+-----+-----+-----+-----+ 1020
 GGTGCGCCCGCGGCTAGGTGTAGCGCGGTGGTGCAGGAACCTGTGCGGAACAGGGCGC

a P R C P P I H I A A T T S W D T F C P P -
 b H A G P P S T S R P P R P G T R L V P E
 c T R A F H P H R G H H V L G H A L S P G -

GTGTAGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGNACACTGCGNCCCTC
 1021 -----+-----+-----+-----+-----+ 1080
 CACATGCGGCTCTGTCTTCTGTAAGGAGATGAGGAGTCCGCTGTCTCTGTGACGCGGGGAG

a V Y A E T K H F L Y S S C D K ? T A ? L -
 b C T P R P S T S S T P Q A T ? T L R P S -
 c V R R D Q A L P L L L R R Q ? H C ? P P -

CTTCTACTCAATATATCTGAGGCGCAGCCTGACTGGCGTTCCGGAGGTTCTGTGAGACA
 1081 -----+-----+-----+-----+-----+ 1140
 GAAGATGAGTTTATATAGACTCCGGGTGGGACGACCGCAAGCCCTCCAGCACCTCTCT

a L P T Q Y I * G P A * L A F G R F V E T
 b F L L N I S E A Q P D W R S G G S W R ? -
 c S Y S I Y L R P S L T G V R E V R G D ? -

NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCGGCGCAGGTTGGCGGCGCTGCCCCA
 1141 -----+-----+-----+-----+-----+ 1200
 NAGAAAGACCAAGGTTCGGAACCTTACGGTCTTAAGGGGGTTCACCGGGGCGACGGGCT

a ? F L V P G L G C Q D S P Q V A P P A P -
 b S F W F Q A L D A R I P R R L P R L P Q -
 c L S G S R P W M P G F P A G C P A C P S -

GCGNCTAGCGCAATGCGGCGCCCTGTTTCTGGAGCTGCTTGGAAACCAAGCGCAGTGCCT
 1201 -----+-----+-----+-----+-----+ 1260
 GCGNATACCGTTTACGCGCGGACAAAGACTTCGACGAACCTTGGTGGCGGCTCACGGG

a A ? L A N A A P V S G A A W E P R A V P -
 b R Y W Q M R F L F L E L L G N H A Q C P -
 c ? T G K C G P C F W S C L G T T R S A P -

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FIGURE 51 (cont.)

CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCCGAGTGCGGTACCCCCAGCAGGCGG
1261 ----- 1320
GATGCCCCACAAAGGAGTTCTGCGTGAAGGGGACGCTCGAAXCAGTGGGGTGTGCGC
a L R G V P Q D A L F A A S C G H F S S R -
b Y G V F L K T H C P L R A A V T F A A G -
c T G C S S R R T A R C E L R S P Q Q P V -
TGTCTGTGCGGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCGAGGAGGAGAACACAG
1321 ----- 1380
ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCGGGGGCTCTCTCTCTTGTGTG
a C L C P G E A P G I C G G P R G G G T Q -
b V C A K E K P Q G S V A A P E E E E H R -
c S V P G R S P R A I W R P F R R R N T D -
ACCCCCGTGCCCTGGTGCAGCTGCTCCGCGAGCACAGCAGGCGCTTGGCAGGTGTACGGCT
1381 ----- 1440
TGGGGGCGCGGACCACGTGCGAGGCGGTCTGTGTGTGCGGGACCGTCCACATGCGGA
a T P V A W C S C S A S T A A P G R C T A -
b P P S P G A A A P P A Q Q P L A G V R L -
c P R R L V Q L L R Q H S S P W Q V Y G F -
TGTGCGGGGCTGCTCGCGCGGCTGTGCGGCCAGGGCTCTGCGGCTCCAGGCACAAAG
1441 ----- 1500
AGCAAGCGCGGAGCGAAGCGGGCGAGCCAGGGGTCCCGAGACCCCGAGGTCTGCTGTG
a S C G P A C A G W C P Q A S G A F G T T -
b R A G L P A P A G A P R P L G I Q A Q R -
c V R A C L R R L V P P G L W G S R H N E -
AAGCGCGCTTCTCTAGGAACACCAAGAAGTTCATCTCTCTGGGGAAGCATGCCAAGCTCT
1501 ----- 1560
TTGCGCGGAAGGAGTCTTGTGTTCTTCAACTAGAGGGACCCCTTCGTACGGTTCCGAGA
a N A A S S G T P R S S S P W G S M P S S -
b T P L P Q E H Q E V H L P G E A C Q A L -
c R R F L R N T K K F I S L G K H A K L S -
CGCTGCGAGAGCTGACGTGGAAGATGAGCGTGGCGGACTGGGCTTGGCTGCCCGAGAGCC
1561 ----- 1620
GCGAGTCTCTGACTGCACCTTCTACTCGCACGCCGTGACCGGAACCGACGCTCTCTGG
a R C R S * R G R * A C G T A L C C A G A -
b A A G A D V E D E R A G L R L A A Q E P -
c L Q E L T W K M S V R D C A W L R R S P -
CAGGGGTGGCTGTGTTCCGGCGCGCAAGCACCGTCTGCGTACGAGATCTGGCCAAGT
1621 ----- 1680
GTCCCCAACCGACACAAAGGCGGGGTCTGTGCGAGACGCACTCTCTAGGACCGGTTC
a Q G L A V F R P Q S T V C V R R S W F S -
b R G W L C S C R R A T S A * G D P G Q V -
c G V G C V F A A E H R L R E E I L A K -

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FIGURE 51 (cont.)

TCCTGCACTGCGTCAAGAGTGTGTAAGTCTGCTGAGCTGCTCAGGTCTTTCTTTTATGTCA
 1681 -----+----- 1740
 AGGACGTGACCGACTACTACACATCCAGCAGCTCGACGAGTCCAGAAACAAAATACAGT

a S C T G * V C T S S S C S C L S F H S -
 b F A L A D E C V K R R A A Q V F L L C H -
 c L H W I M S V Y V V E L L R S F F Y V T -

CGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAGCAAGT
 1741 -----+----- 1800
 GCCCTCGGTGCAAAAGTTTCTTCTGTCGAGAAAAGATCGCCTTCTCACAGACCTGCTTCA

a R R P R F K R T G S F S T G R V S G A S -
 b G D H V S K E Q A L F L P E E C L E Q V -
 c E T T F Q K N R L F F Y R K S V W S K L -

TGCAAAACCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGSAG
 1801 -----+----- 1860
 ACGTTTGTAACTTAGTCTGTCTGAACTTCTCCCAAGTCCAGCCCTGACAGCCTTC

a C K A L E S D S T * R G C S C G S C R K -
 b A K H W N Q T A L E E C A A A C A V G S -
 c Q S T G T R Q H L K R V Q L R E L S E A -

CAGAGGTACAGCAGCATCGCGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCGGCTTCA
 1861 -----+----- 1920
 GTCTCCAGTCCGCTGTAGCCCTTCGCTCGGGCGGGAGCACTCCAGGTCTCAAGCCCAAGT

a Q R S G S I G K P G P P C * R F D S A S -
 b R G Q A A S C S Q A R P A D V Q T P L H -
 c E V R Q H R E A R P A L L T S R L R F I -

TCCCCAGCCTGACGGGCTGCGGCGGATTGTGAACATGGACTACGTGCTGGGAGCCAGAA
 1921 -----+----- 1980
 AGGCGTTCCGACTGCCCCGACGCCGCTAACACTTGT/CCTGATGACAGCACCTCGGTCTT

a S P S L T G C G R L * T W T T S W E P E -
 b P Q A * R A A A D C E H G L R R G S Q N -
 c P K P D G L R P I V N M D Y V V G A R T

CGTTCCGACAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTGTTCAGGG
 1981 -----+----- 2040
 GCAAGGCTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCCG

a R S A E K R C P S V S P E G * R H C S A -
 b V P Q R K E G R A S H L E G E G T V Q R -
 c F R R E K R A E R L T S R V K A L F S V -

TGCTCACTACGACCGCGCGCGCGCTCCGCGCTCTCTGGCGGCTCTGTGCTGGGCTCG
 2041 -----+----- 2100
 ACGAGTTGATCTGCGCGCGCGCGCGCGCGCGCGAGCACCGGAGACAGGACCGGAGC

a C S T T S G R G A P A S W A P L C W A W -
 b A Q L R A G A A P R P P G R I C A G P G -
 c L N Y E R A R R P G L L G A S V L G I D -

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FIGURE 51 (cont.)

ACGATATCCACAGGCGCTGGCGCACCTTGTGCTGCGGTGTGCGGGGCCAGGACCCGCCCC
 2101 -----+-----+-----+-----+-----+ 2150
 TGCTATAGGTGTCCCGGACCGGTGGAAGCAAGCAACGACACGCGCGGTCTCTGGGCGTGG

a T I S T G P G A P S C C V C G P R T R R -
 b R Y F Q G L A H L R A A C A G P G P A A -
 c D I H R A W R T F V L R V R A Q D P P P -

CTGAGCTGTACTTTGTCAAGGTGGATGTGAGCGCGCGGTACGACACCATCCCCAGGACA
 2161 -----+-----+-----+-----+-----+ 2220
 GACTCGACATGAACAGTTCCACCTTACACTGCCCGGCGCATGCTGTGGTAGGGGGTCTCT

a L S C T L S R W M * R A R T T P S F R T -
 b * A V L C Q G G C D G R V R H H P P G Q
 c E L Y F V K V D V T G A Y D T I P Q D R -

GCCACCGAGGTGATGCGCAGCATCATCAACCCAGAACACGTACTGCGTGCCTCGGT
 2221 -----+-----+-----+-----+-----+ 2280
 CCGAGTGCCTCCAGTAGCGGTCTAGTAGTTTGGGTCTTGTGCATGACGCAAGCAGGCA

a G S R R S S P A S S N P R T R T A C V R -
 b A H G G H R Q H H Q T P E H V L R A S V -
 c L T E V I A S I I K P Q N T Y C V R R Y -

ATGCGGTGGTCCAGAACGCCCCCATGGGCACGTCCGCAAGGCGCTTCAGAGGCCAGTCT
 2281 -----+-----+-----+-----+-----+ 2340
 TAGCGCACCAGGTCTTCGCGCGGTACCCGTGCAGGCGTTCGGAAGTTCCTCGGTGCAGA

a M P W S R R P P M G T S A R P S R A T S -
 b C R G P E C R P W A R P Q G L Q E P R L -
 c A V V Q K A A H G H V R K A F K S H V S

CTACCTTGACAGAGCTCCACCGGTACATGCCACAGTTCTTGCTCACTGCAGGANAACA
 2341 -----+-----+-----+-----+-----+ 2400
 GATGGAAGTGTCTGGAGGTGGCATGTACGCTGTCAAGCACCGAGTGGACGTCTCTTTTGT

a L P * Q T S S R T C D S S W L T C R ? T -
 b Y L D R P P A V H A T V R G S P A G ? Q -
 c T L T D L Q P Y M R Q P V A H L Q ? N S -

GCCCCGTCAAGGATCCCGTGTGATGAGCAGAGCTCTCCCTGAATGAGGCCAGCAATG
 2401 -----+-----+-----+-----+-----+ 2460
 CCGGCGACCTCTTACGGCAGCAGTAGCTCTCTCGAAGAGGACTTACTCCGGTCTCTAC

a A R * G M P S S S S R A P P * M R P A V -
 b P A E G C R R H R A E L L P E * G Q Q W -
 c P L R D A V V I E Q S S S L N E A S S G -

GCCCTTCGACGCTCTCTTACGCTTCATCTGCCACCGCGGTGCGCATCAGGGGCAAGT
 2461 -----+-----+-----+-----+-----+ 2520
 CCGAGAGCTGCAGAGGATGCGAAGTACACGGTGGTGGGCAAGGTAGTCCCGGTTC

a A S S T S S Y A S C A T T P C A S G A S -
 b P L R R L P T L H V P P R R A H Q G Q V -
 c L F D V F L R F M C H H A V R I R G K S -

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116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110

[illegible]

[illegible][illegible]

[illegible]

A U G E S R G R R * I F W P P Q F T R H C -
 U S E A P G D D A D C P G G R S Q P G T A -
 C R K L E G T T L T A L E A A A N F A L F -

A P Q T S R P S W T D G H P P T A R P R A -
 B L R L Q D H P G L M A T E P Q T G R E Q -
 C S D F K T I L D * W P F A H S Q A E S R -

D T S S F V T P G S T S Q G G R G G P H -
 T F A A L S R R A L R P K E S G A A H T -
 H Q Q P C H A G L Y V P G R E G R F T F

A P G P H R W E S E A * V S V W P R P A C -
B Q A R T A G S L R P E * V F G R G L H V -
C K P A P L G V * G L S E C L A E A C M S -

A P A E G * V S G * G L S E C P A K C * V
B R L F A E C P A E A * A S V Q P R A E C
C G * R L S V R L R P E R V S S Q G L S V

A S S T P A V F T S P Q A G A R L H F R A
L P A H L P S S L P H R L A L G S T P G P
C O H T C R L H F P T G W R S A F P Q G Q

A S F S S P G A R L P L P T * E * S T P E
B A F P H Q E F G F H S P H R N S P S P D
C L F L T R S P A S T P H I G I V H F Q T

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 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130
 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140
 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150
 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160
 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170
 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180
 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190
 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200
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 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360
 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370
 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380
 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390
 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400
 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410
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 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510
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 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600
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 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640
 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650
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 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670
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 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750
 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760
 1761 1762 1763 1764 1765 1766 1767 1768 1

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1      F A I V H P S P C P P L P S T P T I Q V -
b      S E L F T P R P A L L C L P P P P S R W -
c      P H C S P L A L P S F A F H P H H P G G -

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A T L E R T L G A L G I W S D Q R C A L -
 B P P * E G P W E L W E F G V T A G V P C -
 C D P E K D F G S S G N L E * P K V C P V -

A Y T G E D P A P G W G S L W V K L G G C -
 B T O A R T L H L D G G P C G S N W G E V -
 C H R R C P C T W M C V P V S O I G G E C

A V G V K Y * I Y E F F S F E K K K K K
L W E * N T E Y M S F S V L K K K K K K
C G S K J L N I * V F Q F * K K K K K K -

a	K	K	K	-
b		K	K	-
c			K	K

FIGURE 52

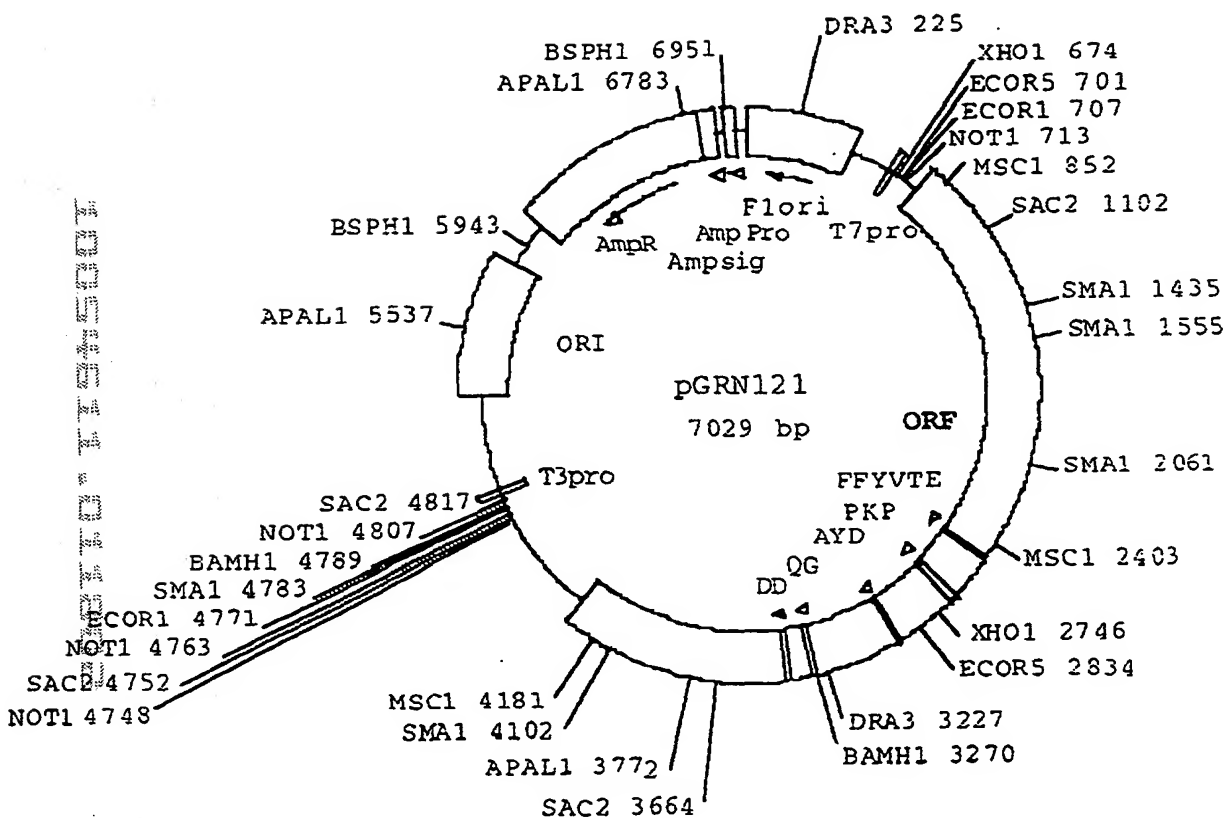


FIGURE 53

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
↑

130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

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FIGURE 53 (cont.)

			140										150			
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his		
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC		
								160								
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys		
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC		
			170										180			
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala		
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC		
								190								
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg		
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	CGA	AGG	CGT		
			200										210			
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly		
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG		
								220								
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly		
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC		
			230										240			
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly		
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC		
								250								
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp		
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG		
			260										270			
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys		
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT		
								280								
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu		
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG		

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

290														300	
gly	ala	leu	ser	gly	thr	arg	his	ser	his	pro	ser	val	gly	arg	
GGT	GCG	CTC	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC	
310															
gln	his	his	ala	gly	pro	pro	ser	thr	ser	arg	pro	pro	arg	pro	
CAG	CAC	CAC	GCG	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC	
320														330	
trp	asp	thr	pro	cys	pro	pro	val	tyr	ala	glu	thr	lys	his	phe	
TGG	GAC	ACG	CCT	TGT	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC	
340															
leu	tyr	ser	ser	gly	asp	lys	glu	gln	leu	arg	pro	ser	phe	leu	
CTC	TAC	TCC	TCA	GGC	GAC	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA	
350														360	
leu	ser	ser	leu	arg	pro	ser	leu	thr	gly	ala	arg	arg	leu	val	
CTC	AGC	TCT	CTG	AGG	CCC	AGC	CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG	
370															
glu	thr	ile	phe	leu	gly	ser	arg	pro	trp	met	pro	gly	thr	pro	
GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	CCC	TGG	ATG	CCA	GGG	ACT	CCC	
380														390	
arg	arg	leu	pro	arg	leu	pro	gln	arg	tyr	trp	gln	met	arg	pro	
CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	TAC	TGG	CAA	ATG	CGG	CCC	
400															
leu	phe	leu	glu	leu	leu	gly	asn	his	ala	gln	cys	pro	tyr	gly	
CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	CAG	TGC	CCC	TAC	GGG	
410														420	
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro	
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA	
430															
ala	ala	gly	val	cys	ala	arg	glu	lys	pro	gln	gly	ser	val	ala	
GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	TCT	GTG	GCG	

FIGURE 53 (cont.)

440 450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

U15444.10.0000

[illegible]

his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 53 (cont.)

770													780		
thr	asp	leu	gln	pro	tyr	met	arg	gln	phe	val	ala	his	leu	gln	
ACA	GAC	CTC	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	
790															
glu	thr	ser	pro	leu	arg	asp	ala	val	val	ile	glu	gln	ser	ser	
GAG	ACC	AGC	CCG	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	
800															
ser	leu	asn	glu	ala	ser	ser	gly	leu	phe	asp	val	phe	leu	arg	
TCC	CTG	AAT	GAG	GCC	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CCG	
810															
phe	met	cys	his	his	ala	val	arg	ile	arg	gly	lys	ser	tyr	val	
TTC	ATG	TGC	CAC	CAC	GCC	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	
820															
gln	cys	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	
CAG	TGC	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	
830															
cys	ser	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	
TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	
840															
ile	arg	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	
ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	
850															
leu	val	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	
TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	
860															
leu	val	arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	
CTG	GTG	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	
870															
lys	thr	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	
AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	
880															
thr	ala	phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	
ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	
890															
900															
910															
920															
930															

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FIGURE 53 (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

1005441.01402

FIGURE 53 (cont.)

1100 1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCCGCCACACCC
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
GGCTGAAGGCTGAGTGTCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
CGCCATTGTTACCCYTCGCCCTGCCYTCTTTGCCTTCCACCCCCACCATCCAGGTGGA
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAA
AAAAAAAAA

1054643433

FIGURE 54

KPN1 17050
KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 23539
SAC1 24607
SAC1 29043

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